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OM protein - protein search, using sw model

Run on: June 6, 2006, 22:41:51 ; Search time 16 Seconds
(without alignments)
321.656 Million cell updates/sec

Title: US-10-063-537-32

Perfect score: 445

Sequence: 1 MSGRDTILGLIALALSLA.....QQDKHSIRNEEGTELOAIVR 445

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 58871 seqs, 11565156 residues

Word size : 6

Total number of hits satisfying chosen parameters: 222

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Published Applications AA New.*

- 1: /EMC_Celerra_SID33/ptodata/2/pubpaa/US09_NEW_PUB.pbp.*
- 2: /EMC_Celerra_SID33/ptodata/2/pubpaa/US06_NEW_PUB.pbp.*
- 3: /EMC_Celerra_SID33/ptodata/2/pubpaa/US07_NEW_PUB.pbp.*
- 4: /EMC_Celerra_SID33/ptodata/2/pubpaa/US08_NEW_PUB.pbp.*
- 5: /EMC_Celerra_SID33/ptodata/2/pubpaa/PCT_NEW_PUB.pbp.*
- 6: /EMC_Celerra_SID33/ptodata/2/pubpaa/US10_NEW_PUB.pbp.*
- 7: /EMC_Celerra_SID33/ptodata/2/pubpaa/US11_NEW_PUB.pbp.*
- 8: /EMC_Celerra_SID33/ptodata/2/pubpaa/US60_NEW_PUB.pbp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	445	100.0	445	6	US-10-196-749-148 Sequence 148, Appl
2	445	100.0	445	7	US-11-101-316-32 Sequence 32, Appl
3	8	1.8	184	6	US-10-953-349-34460 Sequence 34460, A
4	7	1.6	134	6	US-10-953-349-30350 Sequence 30350, A
5	7	1.6	213	7	US-11-293-697-4111 Sequence 4111, Ap
6	7	1.6	218	6	US-10-953-349-22764 Sequence 22764, A
7	7	1.6	332	6	US-10-953-349-10360 Sequence 10360, A
8	7	1.6	357	6	US-10-953-349-10359 Sequence 10359, A
9	7	1.6	368	6	US-10-953-349-22763 Sequence 22763, A
10	7	1.6	391	6	US-10-953-349-22762 Sequence 22762, A
11	7	1.6	405	6	US-10-953-349-3312 Sequence 3312, Ap
12	7	1.6	468	6	US-10-511-937-2595 Sequence 2595, Ap
13	7	1.6	469	6	US-10-953-349-3311 Sequence 3311, Ap
14	7	1.6	471	6	US-10-953-349-10358 Sequence 10358, A
15	7	1.6	496	6	US-10-953-349-3310 Sequence 3310, Ap
16	7	1.6	1122	6	US-10-953-349-7840 Sequence 7840, Ap
17	7	1.6	1147	6	US-10-953-349-7839 Sequence 7839, Ap
18	7	1.6	1211	6	US-10-953-349-7838 Sequence 7838, Ap
19	6	1.3	9	7	US-11-140-487A-1382 Sequence 1382, Ap
20	6	1.3	10	7	US-11-140-487A-1149 Sequence 1149, Ap
21	6	1.3	10	7	US-11-140-487A-1187 Sequence 1187, Ap
22	6	1.3	10	7	US-11-140-487A-1367 Sequence 1267, Ap
23	6	1.3	10	7	US-11-140-487A-1383 Sequence 1383, Ap
24	6	1.3	15	7	US-11-140-487A-2169 Sequence 2169, Ap
25	6	1.3	62	6	US-10-953-349-18220 Sequence 18220, A

RESULT 1

US-10-196-749-148

; Sequence 148, Application US/10196749

; Publication No. US20060094864A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE REFERENCE: P34301C340

; CURRENT FILING DATE: 2002-07-16

; PRIOR FILING DATE: 2002-01-15

; PRIOR APPLICATION NUMBER: 60/052586

; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/059263

; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/059266

; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/063120

; PRIOR FILING DATE: 1997-10-24

; PRIOR APPLICATION NUMBER: 60/063121

; PRIOR FILING DATE: 1997-10-24

; PRIOR APPLICATION NUMBER: 60/063486

; PRIOR FILING DATE: 1997-10-21

; PRIOR APPLICATION NUMBER: 60/063540

; PRIOR FILING DATE: 1997-10-28

; PRIOR APPLICATION NUMBER: 60/063541

; PRIOR FILING DATE: 1997-10-28

; PRIOR APPLICATION NUMBER: 60/063544

; PRIOR FILING DATE: 1997-10-28

; PRIOR APPLICATION NUMBER: 60/063544

; PRIOR FILING DATE: 1997-10-28

; PRIOR APPLICATION NUMBER: 60/063544

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; PRIOR APPLICATION NUMBER: 60/063544

; PRIOR FILING DATE: 1997-10-28

; PRIOR APPLICATION NUMBER: 60/063544

; PRIOR FILING DATE: 1997-10-28

Sequence 34566, A
Sequence 10513, A
Sequence 18287, A
Sequence 3382, Ap
Sequence 30729, A
Sequence 2685, Ap
Sequence 37632, A
Sequence 12280, A
Sequence 20413, A
Sequence 37586, A
Sequence 8614, Ap
Sequence 10512, A
Sequence 2923, Ap
Sequence 28044, A
Sequence 37631, A
Sequence 12279, A
Sequence 18286, A
Sequence 3328, Ap
Sequence 8613, Ap
Sequence 25282, A

	Query Match	100.0%;	Score 445;	DB 6;	Length 445;
	Best Local Similarity	100.0%;	Pred. No. 0;		
	Matches 445;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MSGRDTILGCIILALALSLAMMTEFRITILLVHIFISLVLTGLLFCVGVLMWLYDYDTN	60		
Db	1	MSGRDTILGCIILALALSLAMMTEFRITILLVHIFISLVLTGLLFCVGVLMWLYDYDTN	60		
QY	61	DLSGIELTERENMKCVLGFIAVSTGITAVLLVLI FVLVKRIKLTVELFQITNKAISSAPF	120		
Db	61	DLSGIELTERENMKCVLGFIAVSTGITAVLLVLI FVLVKRIKLTVELFQITNKAISSAPF	120		
QY	121	LLFPQLWTFAILFFFWLWVAVLLSLGTAGAAQWMEGGQVEYKPLSGIRYMWSHLIGLI	180		
Db	121	LLFPQLWTFAILFFFWLWVAVLLSLGTAGAAQWMEGGQVEYKPLSGIRYMWSHLIGLI	180		
QY	181	WTSEFILAQQMTIAGAVVTCYFNRSKNDDPDHPILSSLSILPPYHOGTVVKGSEFLISVV	240		
Db	181	WTSEFILAQQMTIAGAVVTCYFNRSKNDDPDHPILSSLSILPPYHOGTVVKGSEFLISVV	240		
QY	241	RIPRIIVMYMQUALKEQHGALSGYLPRCCYCCFWCLDKVLLHLNQNAYTTTAINGTDFC	300		
Db	241	RIPRIIVMYMQUALKEQHGALSGYLPRCCYCCFWCLDKVLLHLNQNAYTTTAINGTDFC	300		
QY	301	TSKADAFKILSKNSSHFTSINCFGDFPIIFLGKVLVVCFTVFGGLMAFNYNRAFOVWAVPL	360		
Db	301	TSKADAFKILSKNSSHFTSINCFGDFPIIFLGKVLVVCFTVFGGLMAFNYNRAFOVWAVPL	360		
QY	361	LLVAFAYLVAHGSFLSVFEVTLDAFLCFAVDLETNDGSEKPKPFMDQEFLSFVKRSNKL	420		
Db	361	LLVAFAYLVAHGSFLSVFEVTLDAFLCFAVDLETNDGSEKPKPFMDQEFLSFVKRSNKL	420		
QY	421	NNARAQDKHSLRNEEGTELQAIIVR	445		
Db	421	NNARAQDKHSLRNEEGTELQAIIVR	445		

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RESULT 2
US-11-101-316-32
/ Sequence 32, Application US/11101316
/ Publication No. US2006009657A1
/ GENERAL INFORMATION:
/ APPLICANT: Goddard,Audrey J.
/ APPLICANT: Godowski,Paul J.
/ APPLICANT: Grimaldi,Christopher J.
/ APPLICANT: Gurney,Austin L.
/ APPLICANT: WOOD,William I.
/ TITLE OF INVENTION: ANTIBODIES TO A
/ TITLE OF INVENTION: UNDEREXPRESSED
/ FILE REFERENCE: P3230R1C17C1
/ CURRENT APPLICATION NUMBER: US/11/1
/ CURRENT FILING DATE: 2005-04-06
/ PRIOR APPLICATION NUMBER: 10/063526
/ PRIOR FILING DATE: 2002-05-03
/ PRIOR APPLICATION NUMBER: 10/006867
/ PRIOR FILING DATE: 2001-12-06
/ PRIOR APPLICATION NUMBER: PCT/US00/
/ PRIOR FILING DATE: 2000-08-24
/ PRIOR APPLICATION NUMBER: 09/380137
/ PRIOR FILING DATE: 1999-08-25
/ PRIOR APPLICATION NUMBER: PCT/US99/
/ PRIOR FILING DATE: 1999-06-02
/ PRIOR APPLICATION NUMBER: 60/087759
/ PRIOR FILING DATE: 1998-06-02
/ NUMBER OF SEQ ID NOS: 170
/ SEQ ID NO 32
/ LENGTH: 445
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-11-101-316-32

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Query Match 100.0%; Score 445; DB 7; Length 445;

[illegible]

Qy 357 AVPLLLVA 364
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Db 122 AVPLLLVA 129

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RESULT 4
US-10-953-349-30350
; Sequence 30350, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED
; TITLE OF INVENTION: SEQUENCE-DETERMINED
; TITLE OF INVENTION: SEQUENCE-DETERMINED
; FILE REFERENCE: 2750-1579PUS2
; FILE REFERENCE: 2750-1579PUS2

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RESULT 3
US-10-953-349-34460
; Sequence 34460, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 34460
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-10-953-349-34460

Query Match      1.8%; Score 8; DB 6; Length 184;
Best Local Similarity 100.0%; Pred.No.1.4;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      357 AVPLLLVA 364
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Db      122 AVPLLLVA 129

RESULT 4
US-10-953-349-30350
; Sequence 30350, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2

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; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 30350
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-953-349-30350

Query Match 1.6%; Score 7; DB 6; Length 134;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 112 NKAISSA 118
Db 5 NKAISSA 11
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RESULT 5
US-11-293-697-4111
; Sequence 4111, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4111
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-4111

Query Match 1.6%; Score 7; DB 7; Length 213;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 ILGLLFV 47
Db 43 ILGLLFV 49
|||||

RESULT 6
US-10-953-349-22764
; Sequence 22764, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22764
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-22764

Query Match 1.6%; Score 7; DB 6; Length 218;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 229 TVVKGsf 235
|||||

Db 113 TVVKGsf 119

RESULT 7
US-10-953-349-10360
; Sequence 10360, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10360
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-10360

Query Match 1.6%; Score 7; DB 6; Length 332;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 CILALAL 17
Db 135 CILALAL 141
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RESULT 8
US-10-953-349-10359
; Sequence 10359, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10359
; LENGTH: 357
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-10359

Query Match 1.6%; Score 7; DB 6; Length 357;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 CILALAL 17
Db 160 CILALAL 166
|||||

RESULT 9
US-10-953-349-22763
; Sequence 22763, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22763

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; LENGTH: 368
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-22763

Query Match          1.6%; Score 7; DB 6; Length 368;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 229 TVVKGSP 235
Db 263 TVVKGSP 269
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RESULT 10
US-10-953-349-22762
; Sequence 22762, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22762
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-22762

Query Match          1.6%; Score 7; DB 6; Length 391;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 229 TVVKGSP 235
Db 286 TVVKGSP 292
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RESULT 11
US-10-953-349-3312
; Sequence 3312, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3312
; LENGTH: 405
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-3312

Query Match          1.6%; Score 7; DB 6; Length 405;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 CILALAL 17
Db 202 CILALAL 208
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RESULT 12
US-10-511-937-2595
; Sequence 2595, Application US/10511937
; Publication No. US2006008836A1
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; FILE REFERENCE: 50661200104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2595
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-937-2595

Query Match          1.6%; Score 7; DB 6; Length 468;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 358 VPLLVA 364
Db 250 VPLLVA 256
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RESULT 13
US-10-953-349-3311
; Sequence 3311, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3311
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-3311

Query Match          1.6%; Score 7; DB 6; Length 469;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 CILALAL 17
Db 266 CILALAL 272
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RESULT 14
US-10-953-349-10358
; Sequence 10358, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
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; TITLE OF INVENTION: ENCODED THERBY
 ; FILE REFERENCE: 2750-1579PUS2
 ; CURRENT APPLICATION NUMBER: US/10/953,349
 ; CURRENT FILING DATE: 2004-09-30
 ; NUMBER OF SEQ ID NOS: 40252
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 10358
 ; LENGTH: 471
 ; TYPE: PRT
 ; ORGANISM: Arabidopsis thaliana
 US-10-953-349-10358

Query Match 1.6%; Score 7; DB 6; Length 471;
 Best Local Similarity 100.0%; Pred. No. 35;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 CILALAL 17
 Db 274 CILALAL 280

RESULT 15
 US-10-953-349-3310
 ; Sequence 3310, Application US/10953349
 ; Publication No. US20060107345A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ALEXANDROV, Nikolai et al.
 ; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
 ; FILE REFERENCE: 2750-1579PUS2
 ; CURRENT APPLICATION NUMBER: US/10/953,349
 ; CURRENT FILING DATE: 2004-09-30
 ; NUMBER OF SEQ ID NOS: 40252
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 3310
 ; LENGTH: 496
 ; TYPE: PRT
 ; ORGANISM: Arabidopsis thaliana
 US-10-953-349-3310

Query Match 1.6%; Score 7; DB 6; Length 496;
 Best Local Similarity 100.0%; Pred. No. 36;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 CILALAL 17
 Db 293 CILALAL 299

Search completed: June 6, 2006, 22:45:08
 Job time : 18 secs

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OM protein - protein search, using sw model

Run on: June 8, 2006, 23:45:31 ; Search time 183 Seconds
(without alignments)
1126.397 Million cell updates/sec

Perfect score: 445
Sequence: 1 MSGRDTILGILALALSLA.....QQDKSLRNBEETQLQAIVR 445

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Searched: 2097797 seqs, 463214858 residues

Word size : 6

Total number of hits satisfying chosen parameters: 13561

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1500 summaries

Database : Published Applications AA Main:
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4: /EMC_Celerra_SID33/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
5: /EMC_Celerra_SID33/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
6: /EMC_Celerra_SID33/ptodata/2/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	ID	Description
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562	445	100.0	445	4	US-10-174-587-148 Sequence 148, App
626	445	100.0	445	5	US-10-063-742-32 Sequence 32, Appl
741	445	100.0	445	5	US-10-972-317-32 Sequence 32, Appl
743	445	100.0	445	5	US-10-950-374-177 Sequence 177, App
751	445	100.0	445	6	US-11-102-240-32 Sequence 32, Appl
752	445	100.0	445	6	US-11-103-195-32 Sequence 32, Appl
753	344	77.3	653	4	US-10-062-937B-5 Sequence 5, Appli
754	344	77.3	653	4	US-10-391-399-73 Sequence 73, Appl
755	310	69.7	648	5	US-10-330-773-825 Sequence 825, App
756	215	48.3	275	3	US-09-833-245-1911 Sequence 1911, Ap
757	125	28.3	275	6	US-11-264-096-1911 Sequence 1911, Ap
758	122	27.4	275	3	US-09-833-245-1910 Sequence 1910, Ap
759	122	27.4	275	6	US-11-264-096-1910 Sequence 1910, Ap
760	34	7.6	46	4	US-10-425-115-336095 Sequence 336095,
761	27	6.1	558	5	US-10-330-773-822 Sequence 822, App
762	23	5.2	94	4	US-10-425-115-280712 Sequence 280712,
763	23	5.2	329	4	US-10-220-120-317 Sequence 317, App
764	18	4.0	646	4	US-10-062-937B-10 Sequence 10, Appl
765	18	4.0	646	4	US-10-391-399-78 Sequence 78, Appl
766	11	2.5	301	5	US-10-745-586-174 Sequence 174, App
767	11	2.5	446	3	US-09-726-643-58 Sequence 58, Appl
768	11	2.5	446	4	US-10-042-141-58 Sequence 58, Appl
769	11	2.5	446	5	US-10-919-272-58 Sequence 139, App
770	11	2.5	510	3	US-09-726-643-139 Sequence 139, App
771	11	2.5	510	4	US-10-042-141-139 Sequence 139, App
772	11	2.5	510	5	US-10-919-272-139 Sequence 139, App
773	11	2.5	653	4	US-10-062-937B-9 Sequence 9, Appli

774	11	2.5	653	4	US-10-391-399-77 Sequence 77, Appl
775	11	2.5	654	4	US-10-062-937B-7 Sequence 7, Appli
776	11	2.5	654	4	US-10-391-399-75 Sequence 75, Appl
777	11	2.5	657	4	US-10-176-847-48 Sequence 48, Appl
778	11	2.5	657	5	US-10-753-267-6 Sequence 6, Appli
779	11	2.5	657	6	US-11-080-991-48 Sequence 48, Appl
780	11	2.5	708	4	US-10-106-698-6390 Sequence 6390, Ap
781	9	2.0	184	3	US-09-925-300-956 Sequence 956, App
782	8	1.8	13	3	US-09-754-831A-20 Sequence 20, Appl
783	8	1.8	13	5	US-10-671-317-20 Sequence 20, Appl
784	8	1.8	15	4	US-10-430-685-130 Sequence 130, App
785	8	1.8	24	6	US-11-064-039-27 Sequence 27, Appl
786	8	1.8	24	6	US-11-065-970-39 Sequence 39, Appl
787	8	1.8	24	6	US-11-167-636-39 Sequence 39, Appl
788	8	1.8	35	5	US-10-816-768-3 Sequence 3, Appli
789	8	1.8	70	4	US-10-425-115-216147 Sequence 216147,
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792	8	1.8	103	4	US-10-187-394-11 Sequence 11, Appl
793	8	1.8	103	5	US-10-671-317-12 Sequence 12, Appl
794	8	1.8	103	5	US-10-816-768-50 Sequence 50, Appl
795	8	1.8	103	6	US-11-037-782-164 Sequence 164, App
796	8	1.8	103	6	US-11-097-960-72 Sequence 72, Appl
797	8	1.8	104	2	US-08-260-675-26 Sequence 26, Appl
798	8	1.8	104	3	US-09-852-318A-26 Sequence 26, Appl
799	8	1.8	104	4	US-10-050-050-26 Sequence 26, Appl
800	8	1.8	104	5	US-10-865-514-26 Sequence 26, Appl
801	8	1.8	104	6	US-11-226-555-26 Sequence 26, Appl
802	8	1.8	110	4	US-10-366-345-58 Sequence 58, Appl
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805	8	1.8	119	4	US-10-115-406-16 Sequence 16, Appl
806	8	1.8	119	4	US-10-154-333-18 Sequence 18, Appl
807	8	1.8	119	4	US-10-704-223-16 Sequence 16, Appl
808	8	1.8	120	3	US-09-813-459-16 Sequence 16, Appl
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811	8	1.8	120	3	US-09-872-856-42 Sequence 42, Appl
812	8	1.8	120	4	US-10-335-483-24 Sequence 24, Appl
813	8	1.8	120	4	US-10-463-973-42 Sequence 42, Appl
814	8	1.8	120	4	US-10-593-536-14 Sequence 14, Appl
815	8	1.8	120	4	US-10-758-210-14 Sequence 14, Appl
816	8	1.8	120	5	US-10-997-809-28 Sequence 28, Appl
817	8	1.8	120	5	US-10-991-343-34 Sequence 34, Appl
818	8	1.8	149	4	US-10-424-599-277376 Sequence 277376,
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821	8	1.8	183	4	US-10-321-799-23 Sequence 23, Appl
822	8	1.8	183	4	US-10-428-997A-23 Sequence 23, Appl
823	8	1.8	183	6	US-11-051-568-23 Sequence 23, Appl
824	8	1.8	230	5	US-10-527-500-71 Sequence 71, Appl
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826	8	1.8	472	4	US-10-005-228-7 Sequence 7, Appli
827	8	1.8	472	4	US-10-122-026-17 Sequence 17, Appl
828	8	1.8	472	4	US-10-366-345-35 Sequence 35, Appl
829	8	1.8	472	5	US-10-650-326B-12 Sequence 12, Appl
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831	8	1.8	472	5	US-10-931-198-8 Sequence 8, Appli
832	8	1.8	472	5	US-10-942-042-8 Sequence 8, Appli
833	8	1.8	472	6	US-11-092-353-3 Sequence 3, Appli
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835	8	1.8	473	5	US-10-826-324-25 Sequence 25, Appl
836	8	1.8	559	4	US-10-437-963-128120 Sequence 128120,
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839	8	1.8	671	4	US-10-437-963-128849 Sequence 128849,
840	8	1.8	898	3	US-10-506-454-192 Sequence 192, App
841	8	1.8	898	3	US-09-841-739-11 Sequence 11, Appl
842	8	1.8	898	4	US-10-449-315-11 Sequence 11, Appl
843	8	1.8	898	6	US-11-145-631-11 Sequence 11, Appl
844	8	1.8	1023	4	US-10-282-122A-60535 Sequence 60535, A
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846	8	1.8	1045	3	US-09-815-242-10617 Sequence 10617, A

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851	7	1.6	18	3	US-09-971-490-13	Sequence 13, Appl	924	7	1.6	158	3	US-09-801-944B-169	Sequence 169, App
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854	7	1.6	27	6	US-11-129-741-640	Sequence 640, App	927	7	1.6	165	4	US-10-767-701-35659	Sequence 35659, A
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857	7	1.6	43	3	US-09-974-879-433	Sequence 433, App	930	7	1.6	173	6	US-11-096-568A-27299	Sequence 27299, A
858	7	1.6	43	3	US-09-305-736-433	Sequence 433, App	931	7	1.6	174	4	US-10-767-701-42635	Sequence 42635, A
859	7	1.6	43	3	US-09-818-683-433	Sequence 433, App	932	7	1.6	176	4	US-10-425-115-366786	Sequence 366786, A
860	7	1.6	43	3	US-09-818-683-433	Sequence 433, App	933	7	1.6	179	5	US-10-774-355A-2402	Sequence 2402, Ap
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864	7	1.6	48	3	US-09-838-671-80	Sequence 80, Appl	937	7	1.6	186	4	US-10-424-599-157185	Sequence 157185, A
865	7	1.6	49	3	US-09-881-752A-214	Sequence 214, App	938	7	1.6	187	4	US-10-424-599-167441	Sequence 167441, A
866	7	1.6	52	4	US-10-424-599-213500	Sequence 213500, A	939	7	1.6	190	4	US-10-425-115-341952	Sequence 341952, A
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869	7	1.6	57	4	US-10-437-963-108782	Sequence 108782, A	942	7	1.6	197	4	US-10-425-114-72278	Sequence 72278, A
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878	7	1.6	83	4	US-10-424-599-220341	Sequence 220341, A	951	7	1.6	215	5	US-10-739-930-10381	Sequence 10381, A
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884	7	1.6	95	3	US-09-739-907-178	Sequence 178, App	957	7	1.6	231	4	US-10-051-643-152	Sequence 152, App
885	7	1.6	95	3	US-09-938-671-178	Sequence 178, App	958	7	1.6	231	4	US-10-205-979-27	Sequence 27, Appl
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889	7	1.6	105	4	US-10-424-599-158795	Sequence 158795, A	962	7	1.6	234	4	US-10-365-227-13	Sequence 13, Appl
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892	7	1.6	106	6	US-11-096-568A-27368	Sequence 27368, A	965	7	1.6	240	5	US-10-864-252-552	Sequence 552, App
893	7	1.6	114	5	US-10-773-236-289	Sequence 289, App	966	7	1.6	243	4	US-10-425-115-209870	Sequence 209870, A
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905	7	1.6	128	5	US-10-739-930-5942	Sequence 5942, Ap	978	7	1.6	275	4	US-10-425-115-198574	Sequence 198574, A
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910	7	1.6	139	4	US-10-767-701-40784	Sequence 40784, A	983	7	1.6	294	4	US-10-034-623-12	Sequence 12, Appl
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912	7	1.6	142	6	US-11-072-512-3548	Sequence 3548, Ap	985	7	1.6	294	4	US-10-029-120-12	Sequence 12, Appl
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916	7	1.6	145	4	US-10-425-115-366780	Sequence 366780, A	989	7	1.6	301	4	US-10-282-122A-66608	Sequence 66608, A
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918	7	1.6	146	4	US-10-437-963-191106	Sequence 191106, A	991	7	1.6	302	4	US-10-282-122A-42710	Sequence 42710, A
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995	7	1.6	307	6	US-11-079-463-6054	Sequence 6054, Ap	1068	7	1.6	464	4	US-10-238-075-709	Sequence 709, App
996	7	1.6	309	4	US-10-369-493-12234	Sequence 12234, A	1069	7	1.6	466	3	US-09-815-242-14048	Sequence 14048, A
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1006	7	1.6	328	4	US-10-425-115-273313	Sequence 273313, A	1079	7	1.6	467	6	US-11-185-878-6	Sequence 6, Appli
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1008	7	1.6	333	4	US-10-425-114-57911	Sequence 57911, A	1081	7	1.6	468	4	US-10-226-318-2	Sequence 2, Appli
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1011	7	1.6	340	4	US-10-128-714-8089	Sequence 8089, Ap	1084	7	1.6	468	4	US-10-139-785-1	Sequence 1, Appli
1012	7	1.6	340	4	US-10-425-114-52527	Sequence 52527, A	1085	7	1.6	468	4	US-10-292-486-1	Sequence 1, Appli
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1017	7	1.6	353	5	US-10-732-923-7920	Sequence 7920, Ap	1090	7	1.6	468	4	US-10-480-730-1	Sequence 1, Appli
1018	7	1.6	354	5	US-10-467-657-5634	Sequence 5634, Ap	1091	7	1.6	468	4	US-10-630-329-2	Sequence 2, Appli
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1021	7	1.6	360	5	US-10-732-923-7905	Sequence 7905, Ap	1094	7	1.6	468	5	US-10-986-046-1	Sequence 1, Appli
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1147	7	1.6	559	4	US-10-798-512-111	Sequence 111, App	1220	7	1.6	1280	4	US-10-619-359A-2	Sequence 2, Appli
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1171	7	1.6	747	4	US-10-424-599-189158	Sequence 189158,	1244	6	1.3	9	4	US-10-107-533-746	Sequence 746, App
1172	7	1.6	770	4	US-10-437-963-181869	Sequence 181869,	1245	6	1.3	9	4	US-10-107-533-1216	Sequence 1216, Ap
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1195	7	1.6	896	4	US-10-425-115-253624	Sequence 253624,	1268	6	1.3	10	3	US-09-755-630A-162	Sequence 162, App
1196	7	1.6	908	4	US-10-437-963-163711	Sequence 163711,	1269	6	1.3	10	4	US-10-200-708-415	Sequence 415, App
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US-09-991-181-177

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; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Kijavini, Ivar J.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tamas, Daniel

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE REFERENCE: P2730P1C53

; CURRENT APPLICATION NUMBER: US/09/991,181

; CURRENT FILING DATE: 2001-11-16

; PRIOR APPLICATION NUMBER: 60/049787

; PRIOR FILING DATE: 1997-06-16

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/065186

; PRIOR FILING DATE: 1997-11-12

; PRIOR APPLICATION NUMBER: 60/065311

; PRIOR FILING DATE: 1997-11-13

; PRIOR APPLICATION NUMBER: 60/066770

; PRIOR FILING DATE: 1997-11-24

; PRIOR APPLICATION NUMBER: 60/075945

; PRIOR FILING DATE: 1998-02-25

; PRIOR APPLICATION NUMBER: 60/078910

; PRIOR FILING DATE: 1998-03-20

; PRIOR APPLICATION NUMBER: 60/083322

; PRIOR FILING DATE: 1998-03-20


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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match      100.0%; Score 445; DB 2; Length 445;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 DLSIELTERENKMCVLGFAIVSTGITAVLLVLFVLRKRIKLVFQITNKAISSAPP 120
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Db 121 LLFQPLWTFAILIFFVWLWVAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMWVYHLGLI 180
Qy 181 WTSEFILACQMTTAGAVVTCYFNRSKNDDPDHPILSLSLFPYHOGTVVKGSLISVV 240
Db 181 WTSEFILACQMTTAGAVVTCYFNRSKNDDPDHPILSLSLFPYHOGTVVKGSLISVV 240
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Db 241 RIPRIIVVMQNALKEQHGALSRYLFRCCVCCFWCLDKYLLHLNQAYTTTAINGTDFC 300
Qy 301 TSAKDAFKILSKNSSHFTSINCFDGFIFLGKVLVVCFTVFGGLMAFNYNRAFOVMAVPL 360
Db 301 TSAKDAFKILSKNSSHFTSINCFDGFIFLGKVLVVCFTVFGGLMAFNYNRAFOVMAVPL 360
Qy 361 LLVAFAYLVAHSLFSLVFETVLDALFLCFAVDLETDNGSSEKPYFMDQEFSLFVKRSNKL 420
Db 361 LLVAFAYLVAHSLFSLVFETVLDALFLCFAVDLETDNGSSEKPYFMDQEFSLFVKRSNKL 420
Qy 421 NNARAQDKHSLRNEEGTQLQAVR 445
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RESULT 2
US-09-990-444-177
; Sequence 177, Application US/09990444
; Patent No. 6930170
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey J.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.

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; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C19
; CURRENT APPLICATION NUMBER: US/09/990,444
; CURRENT FILING DATE: 2001-11-14
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; PRIOR APPLICATION NUMBER: 60/088858

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; PRIOR FILING DATE: 1998-06-11
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 ; PRIOR FILING DATE: 1998-07-02
 ; PRIOR APPLICATION NUMBER: 60/091978
 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/091982
 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/092182
 ; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 445; DB 2; Length 445;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	61	DLSEILDTERENMKCVLGFATVSTGITAVLLVLI FVLRKRIKLTVELFQITNKAISSAPF	120
QY	121	LLFQPLWTFAILIFFWVLWVAVLLSGTAGAAQVMEGGQVEYKPLSGIRYMWSYHILGLI	180
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QY	181	WTSEFILACQOMTIAGAVTTCYFNRSKNDDPPDHPILSSLSILFFYHQGTWVKGSELSISVV	240
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QY	241	RJPRIIVTMQNALKEQHQGALSRYLFCRCYCCFWCLDKYLLHLNQNAVYTTTAINGTDFC	300
Db	241	RJPRIIVTMQNALKEQHQGALSRYLFCRCYCCFWCLDKYLLHLNQNAVYTTTAINGTDFC	300
QY	301	TSAKDAFKILSKNSSHFTSINCFGDFIIFLGKVLVVCFTVFGGLMAFNVRAPQWVAVPL	360
Db	301	TSAKDAFKILSKNSSHFTSINCFGDFIIFLGKVLVVCFTVFGGLMAFNVRAPQWVAVPL	360
QY	361	LLVAFAYLVAHSFLSVFETVLDALFLCFAVDLETNDGSSEKPYFMDQSEFLSFVKESNKL	420
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RESULT 3
 US-09-997-333-177
 ; Sequence 177, Application US/09997333
 ; Patent No. 6953836
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David	PRIOR APPLICATION NUMBER: 60/088202
APPLICANT: Desnoyers, Luc	PRIOR FILING DATE: 1998-06-05
APPLICANT: Eaton, Dan L.	PRIOR APPLICATION NUMBER: 60/088212
APPLICANT: Ferrara, Napoleone	PRIOR FILING DATE: 1998-06-05
APPLICANT: Fong, Sherman	PRIOR APPLICATION NUMBER: 60/088217
APPLICANT: Gerber, Hanspeter	PRIOR FILING DATE: 1998-06-05
APPLICANT: Gerritsen, Mary E.	PRIOR APPLICATION NUMBER: 60/088655
APPLICANT: Goddard, Audrey	PRIOR FILING DATE: 1998-06-09
APPLICANT: Godowski, Paul J.	PRIOR APPLICATION NUMBER: 60/088734
APPLICANT: Grimaldi, J. Christopher	PRIOR FILING DATE: 1998-06-10
APPLICANT: Gurney, Austin L.	PRIOR APPLICATION NUMBER: 60/088738
APPLICANT: Kljavin, Ivar J.	PRIOR FILING DATE: 1998-06-10
APPLICANT: Napier, Mary A.	PRIOR APPLICATION NUMBER: 60/088742
APPLICANT: Pan, James	PRIOR FILING DATE: 1998-06-10
APPLICANT: Paoni, Nicholas F.	PRIOR APPLICATION NUMBER: 60/088810
APPLICANT: Roy, Margaret Ann	PRIOR FILING DATE: 1998-06-10
APPLICANT: Stewart, Timothy A.	PRIOR APPLICATION NUMBER: 60/088824
APPLICANT: Tumas, Daniel	PRIOR FILING DATE: 1998-06-10
APPLICANT: Watanabe, Colin K.	PRIOR APPLICATION NUMBER: 60/088826
APPLICANT: Williams, P. Mickey	PRIOR FILING DATE: 1998-06-10
APPLICANT: Wood, William I.	PRIOR APPLICATION NUMBER: 60/088858
APPLICANT: Zhang, Zemin	PRIOR FILING DATE: 1998-06-11
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic	PRIOR APPLICATION NUMBER: 60/088861
FILE REFERENCE: P2730PIC27	PRIOR FILING DATE: 1998-06-11
CURRENT APPLICATION NUMBER: US/09/997,333	PRIOR APPLICATION NUMBER: 60/088876
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PRIOR FILING DATE: 1998-06-05	PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090435	PRIOR APPLICATION NUMBER: 60/090435

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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match      100.0%; Score 445; DB 2; Length 445;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSGRDTLGCILALSLAMMTFFRITLLVHIFSLVILGLFVCGVLWMLYYDYTN 60
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QY 61 DLSIELDTERENMKCVLGFVAVSTGITAVLLVILFVLKRKIKLTVLFOITNKAISSAPP 120
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QY 121 LFPQPLWTFAILFFVWLVAVLLSLGTAGAAQVMGGQVEYKPLSGIRYMWYHLIGLI 180
Db 121 LFPQPLWTFAILFFVWLVAVLLSLGTAGAAQVMGGQVEYKPLSGIRYMWYHLIGLI 180

QY 181 WTSEFILACQOMITAGAVVTCYFNRSKNDDPPDHPILSSLSILFFYHOGTVVKGSLISVV 240
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QY 241 RIPRIIVVMQNALKEQHGALSRFLRCCYCCFWCLDKYLLHLNQNAVYTTTAINGTDFC 300
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QY 301 TSAKDAFKILSKNSGHFTSINCFGDFIIFLGLKVLVVCFTVFGGLMAFNYNRAFOVWAVPL 360
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QY 421 NNARAQODKHSRLNEEGTELOAIVR 445
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RESULT 4
US-09-992-598-177
; Sequence 177, Application US/09992598
; Patent No. 6956108
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
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; APPLICANT: Roy, Margaret Ann
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; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC20
; CURRENT APPLICATION NUMBER: US/09/992,598
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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66	PRIOR FILING DATE: 1998-07-07
67	PRIOR APPLICATION NUMBER: 60/092182
68	PRIOR FILING DATE: 1998-07-09

Query Match	100.0%;	Score 445;	DB 2;	Length 445;
Best Local Similarity	100.0%;	Pred. No. 0;		

APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
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APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PIC60
CURRENT APPLICATION NUMBER: US/09/989, 726
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
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33 PRIOR FILING DATE: 1998-07-02
34 PRIOR APPLICATION NUMBER: 60/091978
35 PRIOR FILING DATE: 1998-07-07
36 PRIOR APPLICATION NUMBER: 60/091982
37 PRIOR FILING DATE: 1998-07-07
38 PRIOR APPLICATION NUMBER: 60/092182
39 PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 445; DB 3; Length 445;
Best Local Similarity 100.0%; Pred. No. 0;
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DB 61 DLSIELTERENKCVLGFPAIVSTGITAVLLVLFVLRKRIKUTVELFQITNKAISSAPF 120
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DB 121 LLFQPLWTFAILIFFWLVWAVLLSLCTAGAAQVMEGGQVEYKPLSGIRYMWVHLIGLI 180
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DB 181 WTSEFILACQMTITAGAVVTCYFNRSKNDPPDHPILSSLSILFFYHOGTVVKGSLISVV 240
QY 241 RIPRIIWMQNALKEQHGALSRYLPRCCYCCFWCLDKYLLHLNQNAVYTTTAINGTDFC 300
DB 241 RIPRIIWMQNALKEQHGALSRYLPRCCYCCFWCLDKYLLHLNQNAVYTTTAINGTDFC 300
QY 301 TSAKDAFKILSKNSHSTSNCFGDFIIFLGKVLVVCFTVFGGLMAFNYNRAFOVAVPL 360
DB 301 TSAKDAFKILSKNSHSTSNCFGDFIIFLGKVLVVCFTVFGGLMAFNYNRAFOVAVPL 360
QY 361 LLVAFFAYLVHAFSLVSFETVLDALFLCFVAVDLETNDGSSSEKPYFMDQEFSLFVKRSNKL 420
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Db 421 NNARAOQDKHSLRNEEGTELQAIVR 445
RESULT 7
US-09-997-514-177
; Sequence 177, Application US/09997514
; Patent No. 7019116
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
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; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC46
; CURRENT APPLICATION NUMBER: US/09/997,514
; CURRENT FILING DATE: 2001-11-15
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; PRIOR APPLICATION NUMBER: 60/088026
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088028

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Db 181 WTSEFILLACQOMTAGAVTTCYFNRSKNDPPDHPILSSLSILRPFYHOGTVVKGSLISVV 240
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Qy 301 TSAKDAFKILSKNSHSTINCFDPIIFLGKVLVWCFTVFGGLMAFNARAFQWAVPL 360
Db 301 TSAKDAFKILSKNSHSTINCFDPIIFLGKVLVWCFTVFGGLMAFNARAFQWAVPL 360
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RESULT 8

US-09-989-728-177

; Sequence 177, Application US/09989728

; Patent No. 7029873

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Deenoyers, Luc

; APPLICANT: Eaton, Dan L.

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; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2730P1C72

; CURRENT APPLICATION NUMBER: US/09/989,728

; CURRENT FILING DATE: 2001-11-20

; PRIOR APPLICATION NUMBER: 60/049787

; PRIOR FILING DATE: 1997-06-16

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RESULT 9
US-09-997-349-177
; Sequence 177, Application US/09997349
; Patent No. 7034106
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey

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APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C37
CURRENT APPLICATION NUMBER: US/09/997,349
CURRENT FILING DATE: 2001-11-15
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 ; PRIOR FILING DATE: 1998-07-09

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Db 181 WTSEFILACQOMTITAGAVTTCYFNRSKNDDPPDHPILSSLSILFFYHOGTVKGSFLISVV 240

Qy 241 RIPRIIWMYMONALKEQOHGALSRYLPRCCYCCFWCLDKYLLHNONAYTTTALNGTDFC 300


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; FILING DATE: 29-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 103,604
; FILING DATE: 06-AUG-1993
; APPLICATION NUMBER: 827,052
; FILING DATE: 28-JAN-1992
; APPLICATION NUMBER: 579,865
; FILING DATE: 07-SEP-1990
; APPLICATION NUMBER: 179,406
; FILING DATE: 08-APR-1988
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5496552-6

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RESULT 14
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; Patent No. 6677432
; GENERAL INFORMATION:
; APPLICANT: Stryker Corporation
; TITLE OF INVENTION: Modified Proteins and DNAs of the TGF-beta Superfamily, Including
; TITLE OF INVENTION: Modified Morphogenic Proteins
; FILE REFERENCE: STK-076
; CURRENT APPLICATION NUMBER: US/09/374,958C
; CURRENT FILING DATE: 1999-08-16
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 2.0
; SEQ ID NO 3
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; ORGANISM: Homo sapiens
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US-09-374-958C-3

Query Match      1.8%; Score 8; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 217 SSLSILFF 224
Db 6 SSLSILFF 13

RESULT 15
US-09-374-936-3
; Sequence 3, Application US/09374936
; Patent No. 6846906
; GENERAL INFORMATION:
; APPLICANT: Oppermann, Hermann
; APPLICANT: Tai, Mei-Sheng
; APPLICANT: McCartney, John
; TITLE OF INVENTION: Modified TGF-beta Superfamily Proteins
; FILE REFERENCE: STK-077
; CURRENT APPLICATION NUMBER: US/09/374,936
; CURRENT FILING DATE: 1999-08-16
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: BMP-3

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US-09-374-936-3

Query Match      1.8%; Score 8; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 217 SSLSILFF 224
Db 6 SSLSILFF 13

Search completed: June 6, 2006, 22:31:03
Job time : 52 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: June 6, 2006, 22:21:11 ; Search time 297 Seconds
(without alignments)
1385.966 Million cell updates/sec

Title: US-10-063-537-32
Perfect score: 445
Sequence: 1 MSGRDTILGLCILALSLA.....QQDKHSLNBEGETLQAIVR 445

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 2849598 seqs, 925015592 residues

Word size : 6

Total number of hits satisfying chosen parameters: 29628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : UniProt 7.2.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	344	77.3	605	2 Q726C5_HUMAN	Q726C5 homo sapien
2	344	77.3	653	1 CTL3_HUMAN	Q8n4m1 homo sapien
3	27	6.1	652	1 CTL3_MOUSE	Q921v7 mus musculus
4	23	5.2	604	1 CTL3_RAT	Q6ay92 rattus norv
5	18	4.0	646	1 CTL1_TORMA	Q9i9b9 torpedo mar
6	18	4.0	651	2 Q63253_XENLA	Q63253 xenopus lae
7	18	4.0	651	2 Q6IR74_XENLA	Q6IR74 xenopus lae
8	11	2.5	94	2 Q4T3N9_TETNG	Q4T3N9 tetraodon n
9	11	2.5	653	1 CTL1_MOUSE	Q6x893 mus musculus
10	11	2.5	656	1 CTL1_RAT	Q8vii6 rattus norv
11	11	2.5	657	1 CTL1_HUMAN	Q8wvi5 homo sapien
12	10	2.2	677	2 Q7Q5E7_ANOGA	Q7Q5E7 anopheles g
13	9	2.0	155	2 Q4H957_9DEIO	Q4H957 deinoceroc
14	9	2.0	263	2 Q9A2U8_CAUCR	Q9A2U8 caulobacter
15	8	1.8	77	2 Q74K77_LACJO	Q74K77 lactobacill
16	8	1.8	77	2 Q8A2U7_BACTN	Q8A2U7 bacteroides
17	8	1.8	85	2 Q4CLR3_TREYCR	Q4CLR3 trypanosoma
18	8	1.8	109	2 Q6MX36_MYCBO	Q6MX36 mycobacteri
19	8	1.8	109	2 Q7UIW5_MYCBO	Q7UIW5 mycobacteri
20	8	1.8	114	1 PDZ11_FIG	Q6itq4 sus scrofa
21	8	1.8	117	2 Q9NSW2_CAEEL	Q9NSW2 caenorhabdi
22	8	1.8	128	2 Q8QFL3_ONCMV	Q8QFL3 oncorhynch
23	8	1.8	132	2 Q3Q2G3_XYLEFA	Q3Q2G3 xylella fas
24	8	1.8	132	2 Q3R644_XYLEFA	Q3R644 xylella fas
25	8	1.8	132	2 Q3RH12_XYLEFA	Q3RH12 xylella fas
26	8	1.8	132	2 Q87DE9_XYLEFT	Q87DE9 xylella fas
27	8	1.8	133	2 Q9PD58_XYLEFA	Q9PD58 xylella fas
28	8	1.8	133	2 Q3Z8F4_DEHEL	Q3Z8F4 dehalococco
29	8	1.8	147	1 LYSC3_SHEEP	Q9tun1 ovis aries
30	8	1.8	152	1 M440_ARATH	P93300 arabidopsis
31	8	1.8	152	2 Q6DR78_ARATH	Q6DR78 arabidopsis

32	8	1.8	157	2 Q8XRT5_RALSO	Q8xrt5 ralstonia s
33	8	1.8	161	2 Q50GU6_9BACT	Q50gu6 uncultured
34	8	1.8	161	2 Q3SJ19_THIDA	Q3sej19 thiobacillu
35	8	1.8	162	2 Q67KS7_SYMTH	Q67ks7 symbiobacte
36	8	1.8	163	2 Q50GJ4_9BACT	Q50gj4 uncultured
37	8	1.8	163	2 Q50GJ5_9BACT	Q50gj5 uncultured
38	8	1.8	163	2 Q50GJ7_9BACT	Q50gj7 uncultured
39	8	1.8	163	2 Q50GU8_9BACT	Q50gu8 uncultured
40	8	1.8	163	2 Q50GU9_9BACT	Q50gu9 uncultured
41	8	1.8	167	2 Q9UIR9_CABEL	Q9uir9 caenorhabdi
42	8	1.8	175	2 Q4X0Y5_ASPFU	Q4x0y5 aspergillus
43	8	1.8	177	2 Q2LI72_9GAMM	Q2li72 crenothrix
44	8	1.8	181	2 Q33X89_9GAMM	Q33x89 shewanella
45	8	1.8	188	2 Q4A884_MYCH7	Q4a884 mycoplasma

ALIGNMENTS

RESULT 1	
Q726C5_HUMAN	
ID	Q726C5_HUMAN PRELIMINARY; PRT; 605 AA.
AC	Q726C5;
DT	01-OCT-2003, integrated into UniProtKB/TrEMBL.
DT	01-OCT-2003, sequence version 1.
DT	07-FEB-2006, entry version 12.
DE	Hypothetical protein SLC44A3.
GN	Name=SLC44A3;
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC	Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	NUCLEOTIDE SEQUENCE.
RC	TISSUE=Colon;
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA	Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA	Fahney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA	Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT	"Generation and initial analysis of more than 15,000 full-length human
RT	and mouse cDNA sequences."
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN	[2]
RP	NUCLEOTIDE SEQUENCE.
RC	TISSUE=Colon;
RG	NIH MGC Project;
RL	Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
CC	-----
CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC	Distributed under the Creative Commons Attribution-NoDerivs License
CC	-----
EMBL	BC053877; AAH53877.1; -; mRNA.
DR	Ensembl; ENSG00000143036; Homo sapiens.
DR	LinkHub; Q726C5; -.
DR	InterPro; IPR007603; DUF580.
DR	PANTHER; PTHR12385; DUF580; 1.
DR	Pfam; PF04515; DUF580; 1.
KW	Hypothetical protein.

SQ SEQUENCE 605 AA; 68047 MW; 1182534F9556DADD CRC64;

Query Match 77.3%; Score 344; DB 2; Length 605;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 444; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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 DB 161 MSGRDITLGLCTIALALSALSMAMTFRTFTLLVHIFISVLGLLFCVGLWLVYDYTN 220

QY 61 DLSIELDERENKMCVLGFAIVSTGITAVLLVLI FVLKRKIKLTVLFQITNKAISSAPP 120
 DB 221 DLSIELDERENKMCVLGFAIVSTGITAVLLVLI FVLKRKIKLTVLFQITNKAISSAPP 280

QY 121 LFLPQLWTFAILLFFVWLVAVLLSGLTAGAAQWEGGVKPLSGIRYMSYHLIGLI 180
 DB 281 LFLPQLWTFAILLFFVWLVAVLLSGLTAGAAQWEGGVKPLSGIRYMSYHLIGLI 340

QY 181 WTSEFLACQOMTITAGAVTVCYFNRSKNDPPDHPILSSLSILFFYHOGTWVKGSLISVV 240
 DB 341 WTSEFLACQOMTITAGAVTVCYFNRSKNDPPDHPILSSLSILFFYHOGTWVKGSLISVV 400

QY 241 RIPRIIVMYMNAKQEQHAGLSRYLFRCCYCCFWCLDKYLLHLNQAVYTTTAINGTDFC 300
 DB 401 RIPRIIVMYMNAKQEQHAGLSRYLFRCCYCCFWCLDKYLLHLNQAVYTTTAINGTDFC 460

QY 301 TSAKDAFKILSKNSHFTSINCDFGFIIFLGKVLVVCFTVFGGLMAFNYNRAFOVWAVPL 360
 DB 461 TSAKDAFKILSKNSHFTSINCDFGFIIFLGKVLVVCFTVFGGLMAFNYNRAFOVWAVPL 520

QY 361 LLVAFAYLVAHGFSLVFETVLDAFLCFADLETNDGSEKPYEWDQFSLSPVKRSNKL 420
 DB 521 LLVAFAYLVAHGFSLVFETVLDAFLCFADLETNDGSEKPYEWDQFSLSPVKRSNKL 580

QY 421 NNARAQDQKHSLSRNEGTELQAIVR 445
 DB 581 NNARAQDQKHSLSRNEGTELQAIVR 605

RESULT 2

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 ID_CTL3_HUMAN STANDARD; PRT; 653 AA.
 AC Q8N4W1; Q6UWT1; Q9BWY7;
 DT 30-AUG-2005, integrated into UniProtKB/Swiss-Prot.
 DT 30-AUG-2005, sequence version 3.
 DT 07-MAR-2006, entry version 15.
 DE Choline transporter-like protein 3 (Solute carrier family 44 member 3).
 GN Name=SLC44A3; Synonyms=CTL3; ORFNames=UNQ558/PRO1115;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RG Human chromosome 1 international sequencing consortium;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC TJSUE=Brain, and Colon;
 RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
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 RA Raha S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McSwain P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.C., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 [3]
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 147-653, AND VARIANT
 RP VAL-438.
 RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
 RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,
 RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
 RA Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heidens S.,
 RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
 RA Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,
 RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
 RA Vandlen R.L., Watanabe C., Wieand D., Woods K., Xie M.-H.,
 RA Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
 RA Wood W.I., Godowski P.J., Gray A.M.;
 RT "The secreted protein discovery initiative (SPDI), a large-scale
 RT effort to identify novel human secreted and transmembrane proteins: a
 RT bioinformatics assessment.";
 RL Genome Res. 13:2265-2270 (2003).
 [4]
 RN IDENTIFICATION, AND NOMENCLATURE.
 RP MEDLINE=20144127; PubMed=10677542; DOI=10.1073/pnas.030339697;
 RA O'Regan S., Traifford E., Ruat M., Cha N., Compaore D., Meunier F.-M.;
 RT "An electric lobe suppressor for a yeast choline transporter mutation
 RT belongs to a new family of transporter-like proteins.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:1835-1840 (2000).
 CC -!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein (By
 CC similarity).
 CC -!- SIMILARITY: Belongs to the CTL (choline transporter-like) family.
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 CC -----
 DR EMBL; AC093429; -; NOT_ANNOTATED_CDS; Genomic_DNA.
 DR EMBL; AL359554; CAC36091.1; -; Genomic DNA.
 DR EMBL; BC033858; AAH33858.2; ALT INIT; mRNA.
 DR EMBL; AV358659; AAQ89022.1; ALT INIT; mRNA.
 DR Ensembl; ENSG00000143036; Homo sapiens.
 DR HGNC; HGNC:28689; SLC44A3.
 DR InterPro; IPR007603; DUF580.
 DR Pfam; PF04515; DUF580; 1.
 KW Membrane; Polymorphism; Transmembrane.
 FT CHAIN 1 653
 FT /FTID=PRO_0000191720.
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 FT TRANSMEM 213 233 Potential.
 FT TRANSMEM 243 263 Potential.
 FT TRANSMEM 284 304 Potential.
 FT TRANSMEM 334 354 Potential.
 FT TRANSMEM 384 404 Potential.
 FT TRANSMEM 428 448 Potential.
 FT TRANSMEM 534 554 Potential.
 FT TRANSMEM 563 583 Potential.
 FT VARIANT 438 438 I -> V (in dbSNP:rs59098).
 FT /FTID=VAR_023405.
 FT CONFLICT 465 465 Missing (in Ref. 1; CAC36091).
 SQ SEQUENCE 653 AA; 73797 MW; 54807C920086427B CRC64;

Query Match 77.3%; Score 344; DB 1; Length 653;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 444; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSGRDITLGLCTIALALSALSMAMTFRTFTLLVHIFISVLGLLFCVGLWLVYDYTN 60
 DB 209 MSGRDITLGLCTIALALSALSMAMTFRTFTLLVHIFISVLGLLFCVGLWLVYDYTN 268

RESULT 3

CTL3 MOUSE	STANDARD;	PRT;	652 AA.
ID CTL3 MOUSE			
AC Q921V7;			
DC 30-AUG-2005,	integrated into UniProtKB/Swiss-Prot.		
DT 30-AUG-2005,	sequence version 2.		
DT 07-MAR-2006,	entry version 27.		
DE Choline transporter-like protein 3 (Solute carrier family 44 member			
3).			
DE Name=Slc44a3; Synonym=SLC44A3;			
DE GN musculusus (Mouse);			
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;			
OC Muridea; Muridae; Murinae; Mus.			
OX NCBI_TaxID=10090;			
CC [1]			
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].			
RC STRAIN=FVB/N; TISSUE=Mammary tumor; DOI=10.1073/pnas.242603899;			
RX MEDLINE=22388257; PubMed=12477932; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA Klusner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,			
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,			
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA Villaton D.K., Muzny D.N., Sodergren E.J., Lu X., Gibbs R.A.,			
RA Fahney J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,			
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA Blakesley A.C., Touchman J.W., Green E.D., Dickson M.C.,			
RA Rodriguez R.C., Grimmer J., Schmutz J., Myers R.M.,			
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,			
RA Schnerch A., Schein J.E., Jones S.J.M., Marra W.A.,			
RT "Generation and initial analysis of more than 15,000 full-length human			
RT and mouse cDNA sequences."			
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			
CC -!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein (By			
CC similarity).			
CC -!- SIMILARITY: Belongs to the CTL (choline transporter-like) family.			
CC -----			
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CC			

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FT TRANSMEM 165 185 /FtId=PRO_0000191722.
FT TRANSMEM 195 215 Potential.
FT TRANSMEM 237 257 Potential.
FT TRANSMEM 286 306 Potential.
FT TRANSMEM 330 350 Potential.
FT TRANSMEM 485 505 Potential.
FT TRANSMEM 514 534 Potential.
SQ SEQUENCE 604 AA; 67679 MW; BA47C3A411CE3E1B CRC64;

Query Match 5.2%; Score 23; DB 1; Length 604;
Best Local Similarity 100.0%; Pred. No. 8.6e-13;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 385 LFLCFAVDLETNDGSSSEKPYFMD 407
Db 544 LFLCFAVDLETNDGSSSEKPYFMD 566
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RESULT 5
CTLI_TORMA STANDARD; PRT; 646 AA.
AC Q91B9;
DT 30-AUG-2005, integrated into UniProtKB/Swiss-Prot.
DT 01-OCT-2000, sequence version 1.
DT 07-FEB-2006, entry version 17.
DE Choline transporter-like protein 1.
GN Names=CTLI;
OS Torpedo marmorata (Marbled electric ray).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squala; Hyposquala; Pristigaster; Batoida;
OC Torpediniformes; Torpedinoidei; Torpedinidae; Torpedo.
OX NCBI_TaxID=7788;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA], AND FUNCTION.
RX MEDLINE=20144127; PubMed=10677542; DOI=10.1073/pnas.030339697;
RA O'Regan S., Traffort E., Ruat M., Cha N., Compaore D., Meunier F.-M.;
RT "An electric lobe suppressor for a yeast choline transport mutation
RT belongs to a new family of transporter-like proteins.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:1835-1840(2000).
RN [2]
RP TISSUE SPECIFICITY, AND SUBCELLULAR LOCATION.
RX PubMed=12352613; DOI=10.1097/00001756-200209160-00009;
RA Meunier F.-M., O'Regan S.;
RT "Expression of CTLI in myelinating structures of Torpedo marmorata.";
RL NeuroReport 13:1617-1620(2002).
RN [3]
RP FUNCTION, AND TISSUE SPECIFICITY.
RX PubMed=12675144; DOI=10.1023/A:1022877524469;
RA O'Regan S., Meunier F.-M.;
RT "Selection and characterization of the choline transport mutation
RT suppressor from Torpedo electric lobe, CTLI.";
RL Neurochem. Res. 28:551-555(2003).
CC -1- FUNCTION: Probable choline transporter. May be involved in
CC membrane synthesis and myelin production.
CC -1- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein.
CC -1- TISSUE SPECIFICITY: Present in myelinated structures from brain
CC and spinal chord (at protein level).
CC -1- SIMILARITY: Belongs to the CTL (choline transporter-like) family.
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CC -----
DR ENBL; A0245618; CAB75556.1; -; mRNA.
DR InterPro; IPR007603; DUF580.
DR PANTHER; PTHR12385; DUF580; 1.
DR Pfam; PF04515; DUF580; 1.
DR Membrane; Transmembrane; Transport.
FT CHAIN 1 646 Choline transporter-like protein 1.
FT /FtId=PRO_0000191715.
FT TOPO_DOM 1 27 Cytoplasmic (Potential).
FT TRANSMEM 28 48 Potential.
FT TOPO_DOM 49 207 Extracellular (Potential).

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FT TRANSMEM 208 228 Potential.
FT TOPO_DOM 229 233 Cytoplasmic (Potential).
FT TRANSMEM 234 254 Potential.
FT TOPO_DOM 255 281 Extracellular (Potential).
FT TRANSMEM 282 302 Potential.
FT TOPO_DOM 303 308 Cytoplasmic (Potential).
FT TRANSMEM 309 329 Potential.
FT TOPO_DOM 330 331 Extracellular (Potential).
FT TRANSMEM 332 352 Potential.
FT TOPO_DOM 353 373 Cytoplasmic (Potential).
FT TRANSMEM 374 394 Potential.
FT TOPO_DOM 395 435 Extracellular (Potential).
FT TRANSMEM 436 456 Potential.
FT TOPO_DOM 457 530 Cytoplasmic (Potential).
FT TRANSMEM 531 551 Potential.
FT TOPO_DOM 552 559 Extracellular (Potential).
FT TRANSMEM 560 580 Potential.
FT TOPO_DOM 581 646 Cytoplasmic (Potential).
FT COMPIAS 467 485 Cys-rich.
SQ SEQUENCE 646 AA; 72254 MW; A19A0E1D81453F6F CRC64;

Query Match 4.0%; Score 18; DB 1; Length 646;
Best Local Similarity 100.0%; Pred. No. 6.3e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 183 SEFILACQOMTIAGAVVT 200
Db 389 SEFILACQOMTIAGAVVT 406
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|||||

RESULT 6
Q63ZS3 XENLA PRELIMINARY; PRT; 651 AA.
ID Q63ZS3_XENLA
AC Q63ZS3;
DT 25-OCT-2004, integrated into UniProtKB/TrEMBL.
DT 25-OCT-2004, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE MGC82240 protein.
GN Name=MGC82240;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Splice;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Splice;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

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RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RA Klein S., Gernhard D.S.;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
CC Copyrighted by the Uniprot Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL: BC082837; AAH82837.1; -; mRNA.
DR InterPro: IPR007603; DUF580.
DR PANTHER: PTHR12385; DUF580; 1.
DR Pfam: PF04515; DUF580; 1.
SQ SEQUENCE 651 AA; 72937 MW; A26613B3055420AF CRC64;

Query Match 4.0%; Score 18; DB 2; Length 651;
Best Local Similarity 100.0%; Pred. No. 6.3e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 183 SEFILACQOMTIAGAVVT 200
DB 392 SEFILACQOMTIAGAVVT 409

RESULT 7
Q6IR74_XENLA
ID Q6IR74_XENLA PRELIMINARY; PRT; 651 AA.
AC Q6IR74;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE MGC82240 protein.
GN Name=MGC82240;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
[1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.;
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toehiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Rouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalley D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strauberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
```

```
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
[3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RA Klein S., Strauberg R.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL: BC071026; AAH71026.1; -; mRNA.
DR InterPro: IPR007603; DUF580.
DR PANTHER: PTHR12385; DUF580; 1.
DR Pfam: PF04515; DUF580; 1.
SQ SEQUENCE 651 AA; 72908 MW; 619A2CB2C848FOAF CRC64;

Query Match 4.0%; Score 18; DB 2; Length 651;
Best Local Similarity 100.0%; Pred. No. 6.3e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 183 SEFILACQOMTIAGAVVT 200
DB 392 SEFILACQOMTIAGAVVT 409

RESULT 8
Q4T3N9_TETNG
ID Q4T3N9_TETNG PRELIMINARY; PRT; 94 AA.
AC Q4T3N9;
DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Chromosome undetermined SCAF9971, whole genome shotgun sequence.
DE (Fragment).
GN ORFNames=GSTENG0000709001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontoidea; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
[1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15496914; DOI=10.1038/nature03025;
RA Jaillon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castellani V., Katinka M., Vacherie B.,
RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.-P., Gouzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.-N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Lundberg V., Schacherer V., Quetier F., Saurin W., Scarpelli C.,
RA Winkler P., Lander E.S., Weissbach J., Roest Crolius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RL the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
[2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -i- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -----
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CC -----
CC EMBL: CAAE01009971; CAF92493.1; -; Genomic_DNA.
DR InterPro: IPR007603; DUF580.
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DR PANTHER; PTHR12385; DUF580; 1.
 FT NON TER 1 1
 SQ SEQUENCE 94 AA; 10554 MW; D9C6AAEF02ED9824 CRC64;
 Query Match 2.5%; Score 11; DB 2; Length 94;
 Best Local Similarity 100.0%; Pred. No. 0.085;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 190 QQMTIAGAVT 200
 Db 59 QQMTIAGAVT 69
 RESULT 9
 CTL1_MOUSE STANDARD; PRT; 653 AA.
 AC Q6X893; Q6X894; Q8ROY4; Q91229;
 DT 30-AUG-2005, integrated into UniProtKB/Swiss-Prot.
 DT 30-AUG-2005, sequence version 2.
 DT 07-MAR-2006, entry version 15.
 DE Choline transporter-like protein 1 (Solute carrier family 44 member 1) (CD92 antigen) (CDw92).
 DE (CD92 antigen) (CDw92).
 GN Name=Slc44a1; Synonyms=Cdw92, Ctl1;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; OC Muridae; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS 1 AND 2), TISSUE SPECIFICITY, SUBCELLULAR LOCATION, AND FUNCTION.
 RC STRAIN=FVB/N; TISSUE=Liver, and Mammary gland;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Klausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausberg R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Diatchenko L., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J., Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: Probable choline transporter. May be involved in membrane synthesis and myelin production.
 CC -!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1; Synonyms=A;
 CC IsoId=Q6X893-1; Sequence=Displayed;
 CC Name=2; Synonyms=B;
 CC IsoId=Q6X893-2; Sequence=VSP_015428;
 CC -!- TISSUE SPECIFICITY: Specifically abundant in skeletal muscle (at protein level).
 CC -!- SIMILARITY: Belongs to the CTL (choline transporter-like) family.

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 CC EMBL; AY249865; AAP81042.1; -; mRNA.
 CC EMBL; AY249866; AAP81043.1; -; mRNA.
 CC EMBL; BC010258; AAH10258.1; -; mRNA.
 CC EMBL; BC025941; AAH25941.1; ALT INIT; mRNA.
 CC Ensembl; ENSMUSG0000028412; Mus musculus.
 CC MGI; MGI:2140592; Slc44a1.
 DR GO; GO:0016021; C:integral to membrane; IDA.
 DR GO; GO:0015220; F:choline transporter activity; IDA.
 DR GO; GO:0015871; P:choline transport; IDA.
 DR InterPro; IPR007603; DUF580.
 DR Pfam; PF04515; DUF580; 1.
 KW Alternative splicing; Membrane; Transmembrane; Transport.
 FT CHAIN 1 653 Choline transporter-like protein 1.
 FT /FTID=PRO_0000191713.
 FT Cytoplasmic (Potential).
 FT Extracellular (Potential).
 FT Potential.
 FT TOPO_DOM 1 29
 FT TRANSMEM 30 50
 FT TOPO_DOM 51 211
 FT TRANSMEM 212 232
 FT TOPO_DOM 233 237
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 FT TOPO_DOM 259 287
 FT TRANSMEM 288 308
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 FT TRANSMEM 315 335
 FT TOPO_DOM 336 337
 FT TRANSMEM 338 358
 FT TOPO_DOM 359 379
 FT TRANSMEM 380 400
 FT TOPO_DOM 401 441
 FT TRANSMEM 442 462
 FT TOPO_DOM 463 536
 FT TRANSMEM 537 557
 FT TOPO_DOM 558 565
 FT TRANSMEM 566 586
 FT TOPO_DOM 587 653
 FT COMPIAS 473 491
 FT VARSPLIC 650 653
 FT LRRK -> VGSBEEAALHDFPHFVSVCVFTDCTSSGEAL
 FT VVCIQTQMLLFILFACLPITWMAEVLSQLRLPSVKVS (in isoform 2).
 FT /FTID=VSP_015428.
 FT L -> P (in Ref. 2; AAH25941).
 FT F -> L (in Ref. 2; AAH25941).
 FT L -> F (in Ref. 2; AAH25941).
 SQ SEQUENCE 653 AA; 73083 MW; 3857DA8BE428EFF5 CRC64;
 Query Match 2.5%; Score 11; DB 1; Length 653;
 Best Local Similarity 100.0%; Pred. No. 0.38;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 183 SEFILACQOMT 193
 Db 395 SEFILACQOMT 405
 RESULT 10
 CTL1_MOUSE STANDARD; PRT; 656 AA.
 AC Q8V1I6; Q9JUZ7;
 DT 30-AUG-2005, integrated into UniProtKB/Swiss-Prot.
 DT 01-MAR-2002, sequence version 1.
 DT 07-MAR-2006, entry version 21.
 DE Choline transporter-like protein 1 (Solute carrier family 44 member 1) (CD92 antigen) (CDw92).
 DE (CD92 antigen) (CDw92).
 GN Name=Slc44a1; Synonyms=Cdw92, Ctl1;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; OC Muridae; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]

RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 2), AND TISSUE SPECIFICITY.
RC TISSUE=Brain;
RX MEDLINE=20144127; PubMed=10677542; DOI=10.1073/pnas.030339697;
RA O'Regan S., Traiffort E., Ruat M., Cha N., Compaore D., Meunier F.-M.;
RT "An electric lobe suppressor for a yeast choline transporter mutation
RT belongs to a new family of transporter-like proteins.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:1835-1840(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1), FUNCTION, AND TISSUE
RP SPECIFICITY.
RC STRAIN=Wistar; TISSUE=Brain;
RX PubMed=15715662; DOI=10.1111/j.1471-4159.2004.02962.x;
RA Traiffort E., Ruat M., O'Regan S., Meunier F.-M.;
RT "Molecular characterization of the family of choline transporter-like
RT proteins and their splice variants.";
RL J. Neurochem. 92:1116-1125(2005).
RN [3]
RP INDUCTION.
RX PubMed=12007839; DOI=10.1016/S0169-328X(02)00182-1;
RA Che Y.H., Yamashita T., Higuchi H., Toyama M.;
RT "Changes in mRNA for choline transporter-like protein following facial
RT nerve transection.";
RL Brain Res. Mol. Brain Res. 101:122-125(2002).
RN [4]
RP FUNCTION, AND TISSUE SPECIFICITY.
RX PubMed=16000150; DOI=10.1111/j.1471-4159.2005.03299.x;
RA Inazu M., Takeda H., Matsumiya T.;
RT "Molecular and functional characterization of an Na-independent
RT choline transporter in rat astrocytes.";
RL J. Neurochem. 94:1427-1437(2005).
RN [5]
RP INDUCTION.
RX PubMed=15691711; DOI=10.1016/j.mcn.2004.09.014;
RA Leconte M.-J., De Gois S., Guerci A., Ravassard P., Faucon Biguet N.,
RA Mallet J., Berrard S.;
RT "Differential expression and regulation of the high-affinity choline
RT transporter CHTL and choline acetyltransferase in neurons of superior
RT cervical ganglia.";
RL Mol. Cell. Neurosci. 28:303-313(2005).
CC -1- FUNCTION: Probable choline transporter. May be involved in
CC membrane synthesis and myelin production.
CC -1- INDUCTION: By leukemia inhibitory factor or retinoic acid in
CC vitro. In vivo, induced during the axonal elongation period
CC following axotomy.
CC -1- SIMILARITY: Belongs to the CTL (choline transporter-like) family.
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CC -----
CC EMBL: AJ245619; CAB75555.1; -; mRNA.
CC EMBL: AJ245619; CAB75555.1; -; mRNA.
CC Ensembl: ENSRNOG0000017846; Rattus norvegicus.
CC RGD: 621426; Cdw92.
CC InterPro: IPR007603; DUF580.
CC PANTHER: PTHR12385; DUF580; 1.
CC Pfam: PF04515; DUF580; 1.
CC Alternative splicing; Membrane; Transmembrane; Transport.
KW Choline transporter-like protein 1.
FT CHAIN 1 656 /FTid=PRO_0000191714.
FT TOPO_DOM 1 29
FT TRANSMEM 30 50
FT TOPO_DOM 51 211
FT TRANSMEM 212 232

FT TOPO_DOM 233 237 Cytoplasmic (Potential).
FT TRANSMEM 238 258 Potential.
FT TOPO_DOM 259 287 Extracellular (Potential).
FT TRANSMEM 288 308 Potential.
FT TOPO_DOM 309 314 Cytoplasmic (Potential).
FT TRANSMEM 315 335 Potential.
FT TOPO_DOM 336 337 Extracellular (Potential).
FT TRANSMEM 338 358 Potential.
FT TOPO_DOM 359 379 Cytoplasmic (Potential).
FT TRANSMEM 380 400 Potential.
FT TOPO_DOM 401 441 Extracellular (Potential).
FT TRANSMEM 442 462 Potential.
FT TOPO_DOM 463 536 Cytoplasmic (Potential).
FT TRANSMEM 537 557 Potential.
FT TOPO_DOM 558 565 Extracellular (Potential).
FT TRANSMEM 566 586 Potential.
FT TOPO_DOM 587 656 Cytoplasmic (Potential).
FT COMPLETAS 473 491 Cys-rich.
FT VARSPLIC 650 653 ASGA -> LRKR (in isoform 2).
FT VARSPLIC 654 656 /FTid=VSP_015429.
FT Missing (in isoform 2).
FT /FTid=VSP_015430.
FT CONFLICT 267 267 R -> S (in Ref. 1).
FT CONFLICT 645 645 K -> E (in Ref. 1).
SQ SEQUENCE 656 AA; 73092 MW; 217AD02F684D138 CRC64;
Query Match 2.5%; Score 11; DB 1; Length 656;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 183 SEFILACQMT 193
DB 395 SEFILACQMT 405
|||||
RESULT 11
CTLI_HUMAN STANDARD; PRT; 657 AA.
ID CTLI_HUMAN Q8WU15; Q8WU15; Q8WU15; Q8WU15; Q8WU15; Q8WU15;
AC Q8WU15; Q8WU15; Q8WU15; Q8WU15; Q8WU15; Q8WU15;
DT 30-AUG-2005, integrated into UniProtKB/Swiss-Prot.
DT 01-MAR-2002, sequence version 1.
DT 07-MAR-2006, entry version 27.
DE Choline transporter-like protein 1 (Solute carrier family 44 member 1
DE (CD92 antigen) (CDW92).
GN Name=SLC44A1; Synonyms=CDW92, CTL1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND ALTERNATIVE SPLICING (ISOFORM
RP 2).
RC TISSUE=Ewing sarcoma;
RX MEDLINE=20144127; PubMed=10677542; DOI=10.1073/pnas.030339697;
RA O'Regan S., Traiffort E., Ruat M., Cha N., Compaore D., Meunier F.-M.;
RT "An electric lobe suppressor for a yeast choline transporter mutation
RT belongs to a new family of transporter-like proteins.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:1835-1840(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 3), AND TISSUE SPECIFICITY.
RX MEDLINE=21555187; PubMed=11698453;
RA Wille S., Szekeres A., Majdic O., Prager E., Staffler G., Stoeckl J.,
RA Kunthaler D., Prieschl E.E., Baumrucker T., Burtscher H.,
RA Zlabinger G.J., Knapp W., Stockinger H.;
RT "Characterization of CDw92 as a member of the choline transporter-like
RT protein family regulated specifically on dendritic cells.";
RL J. Immunol. 167:5795-5804(2001).
RN [3]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1).
RX TISSUE=Ewing sarcoma;
RX PubMed=15715662; DOI=10.1111/j.1471-4159.2004.02962.x;
RA Traiffort E., Ruat M., O'Regan S., Meunier F.-M.;

RT "Molecular characterization of the family of choline transporter-like
 RT proteins and their splice variants.";
 RL J. Neurochem. 92:1116-1125 (2005).
 RN [4]
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RP PubMed=15164053; DOI=10.1038/nature02465;
 RA Humphray S.J., Oliver T.K., Hunt A.R., Plumb R.W., Loveland J.E.,
 RA Ainscough R., Almeida J.P., Ambrose K.D., Searle S., Hunt S.E., Scott C.E., Jones M.C.,
 RA Babbage A.K., Babbage S., Bagguley C.L., Bailey J., Banerjee R.,
 RA Barker D.J., Barlow K.F., Bates K., Beasley H., Beasley O., Bird C.P.,
 RA Bray-Allen S., Brown A.J., Brown J.Y., Burford D., Burrill W.,
 RA Burton J., Carder C., Carter N.P., Chapman J.C., Chen Y., Clarke G.,
 RA Clark S.Y., Clee C.M., Clegg S., Collier R.E., Corby N., Crosier M.,
 RA Cummings A.F., Davies J., Dhani P., Dunn M., Dutta I., Dyer L.W.,
 RA Earthrowl M.E., Faulkner L., Fleming C.J., Frankish A.,
 RA Frankland J.A., French L., Fricker D.G., Garner P., Garnett J.,
 RA Ghori J., Gilbert J.G.R., Gilson C., Grafham D.V., Gribble S.,
 RA Griffiths C., Griffiths-Jones S., Grocock R., Guy J., Hall R.E.,
 RA Hammond S., Harley J.L., Harrison E.S.I., Hart E.A., Heath P.D.,
 RA Henderson C.D., Hopkins B.L., Howard P.J., Howden P.J., Huckle E.,
 RA Johnson C., Johnson D., Joy A.A., Kay M., Keenan S., Kershaw J.K.,
 RA Kimberley A.M., King A., Knights A., Laird G.K., Langford C.,
 RA Lawlor S., Leongamornlert D.A., Leversha M., Lloyd C., Lloyd D.M.,
 RA Lovell J., Martin S., Maehreggi-Mohammadi M., Matthews L., McLaren S.,
 RA McLay K.E., Murray A., Milne S., Nickerson T., Nisbett J.,
 RA Nordieck G., Pearce A.V., Peck A.I., Porter K.M., Pandian R.,
 RA Pellan S., Phillimore B., Povey S., Ramsey Y., Rand V., Scharfe M.,
 RA Sehra H.K., Showkeen R., Sims S.K., Skuce C.D., Smith M.,
 RA Stewart C.A., Swarbreck D., Sycamore N., Tester J., Thorpe A.,
 RA Tracey A., Tromans A., Thomas D.W., Wall M., Wallis J.M., West A.P.,
 RA Whitehead S.L., Willey D.B., Williams S.A., Wilming L., Wray P.W.,
 RA Young L., Ashurst J.L., Coulson A., Blocker H., Durbin R.,
 RA Sulston J.E., Hubbard T., Jackson M.J., Bentley D.R., Beck S.,
 RA Rogers J., Dunham I.;
 RT "DNA sequence and analysis of human chromosome 9";
 RL Nature 429:369-374 (2004).
 RN [5]
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
 RP TISSUE=Eye, and Lung;
 RC MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derje J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan B., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Harte S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 CC -1- FUNCTION: Probable choline transporter. May be involved in
 CC membrane synthesis and myelin production (By similarity).
 CC -1- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein (By
 CC similarity).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=1; Synonyms=A;
 CC IsoId=Q8WWI5-1; Sequence=Displayed;
 CC Name=2; Synonyms=B;
 CC IsoId=Q8WWI5-2; Sequence=VSP_015424, VSP_015425;
 CC Name=3; Synonyms=C;
 CC IsoId=Q8WWI5-3; Sequence=VSP_015426, VSP_015427;

CC -1- TISSUE SPECIFICITY: Expressed in various cells of the
 CC hematopoietic system.
 CC -1- SIMILARITY: Belongs to the CTL (choline transporter-like) family.
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 CC -----
 CC EMBL: AJ245620; CAB75541.2; -; Genomic_DNA.
 DR EMBL: AJ273365; CAC82175.1; -; mRNA.
 DR EMBL: AJ420812; CAD12764.1; -; mRNA.
 DR EMBL: AJ161627; CAI13069.1; -; Genomic_DNA.
 DR EMBL: AL450265; CAI13069.1; JOINED; Genomic_DNA.
 DR EMBL: AL590368; CAI13069.1; JOINED; Genomic_DNA.
 DR EMBL: AL161627; CAI13070.1; -; Genomic_DNA.
 DR EMBL: AL450265; CAI13070.1; JOINED; Genomic_DNA.
 DR EMBL: AL590368; CAI13070.1; JOINED; Genomic_DNA.
 DR EMBL: AL161627; CAI13071.1; -; Genomic_DNA.
 DR EMBL: AL450265; CAI13071.1; JOINED; Genomic_DNA.
 DR EMBL: AL590368; CAI13071.1; JOINED; Genomic_DNA.
 DR EMBL: AL450265; CAI14395.1; -; Genomic_DNA.
 DR EMBL: AL161627; CAI14395.1; JOINED; Genomic_DNA.
 DR EMBL: AL590368; CAI14395.1; JOINED; Genomic_DNA.
 DR EMBL: AL450265; CAI14396.1; -; Genomic_DNA.
 DR EMBL: AL161627; CAI14396.1; JOINED; Genomic_DNA.
 DR EMBL: AL590368; CAI14396.1; JOINED; Genomic_DNA.
 DR EMBL: AL450265; CAI14397.1; -; Genomic_DNA.
 DR EMBL: AL161627; CAI14397.1; JOINED; Genomic_DNA.
 DR EMBL: AL590368; CAI14397.1; JOINED; Genomic_DNA.
 DR EMBL: AL590368; CAH73434.1; -; Genomic_DNA.
 DR EMBL: AL161627; CAH73434.1; JOINED; Genomic_DNA.
 DR EMBL: AL450265; CAH73434.1; JOINED; Genomic_DNA.
 DR EMBL: AL590368; CAH73435.1; -; Genomic_DNA.
 DR EMBL: AL161627; CAH73435.1; JOINED; Genomic_DNA.
 DR EMBL: AL450265; CAH73436.1; -; Genomic_DNA.
 DR EMBL: AL161627; CAH73436.1; JOINED; Genomic_DNA.
 DR EMBL: BC018213; AAH18213.1; -; mRNA.
 DR EMBL: BC049203; AAH49203.1; -; mRNA.
 DR Ensembl: ENSG00000070214; Homo sapiens.
 DR HGNC: HGNC:18798; SLC44A1.
 DR MIM: 606105; gene.
 DR InterPro: IPR007603; DUF580.
 DR PANTHER: PTHR12385; DUF580; 1.
 DR Pfam: PF04515; DUF580; 1.
 KW Alternative splicing; Antigen; Membrane; Transmembrane; Transport.
 FT CHAIN 1 657 Choline transporter-like protein 1.
 FT /FTid=PRO_000019172.
 FT TOPO_DOM 1 30 Cytoplasmic (Potential).
 FT TRANSMEM 31 51 Potential.
 FT TOPO_DOM 52 212 Extracellular (Potential).
 FT TRANSMEM 213 233 Potential.
 FT TOPO_DOM 234 238 Cytoplasmic (Potential).
 FT TRANSMEM 239 259 Potential.
 FT TOPO_DOM 260 288 Extracellular (Potential).
 FT TRANSMEM 289 309 Potential.
 FT TOPO_DOM 310 315 Cytoplasmic (Potential).
 FT TRANSMEM 316 336 Potential.
 FT TOPO_DOM 337 338 Extracellular (Potential).
 FT TRANSMEM 339 359 Potential.
 FT TOPO_DOM 360 380 Cytoplasmic (Potential).
 FT TRANSMEM 381 401 Potential.
 FT TOPO_DOM 402 442 Extracellular (Potential).
 FT TRANSMEM 443 463 Potential.
 FT TOPO_DOM 464 537 Extracellular (Potential).
 FT TRANSMEM 538 558 Potential.
 FT TOPO_DOM 559 566 Extracellular (Potential).
 FT TRANSMEM 567 587 Potential.
 FT TOPO_DOM 588 657 Cytoplasmic (Potential).
 FT COMPBIAS 474 492 Cys-rich.
 FT VARSPPLIC 651 654 ASGA -> LKXR (in isoform 2).
 FT /FTid=VSP_015424.
 FT AS -> IK (in isoform 3).
 FT VARSPPLIC 651 652


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FT  VARSPLIC 653 657 /FTid=VSP_015426.
FT  Missing (in isoform 3).
FT  /FTid=VSP_015427.
FT  VARSPLIC 655 657 Missing (in isoform 2).
FT  /FTid=VSP_015425.
FT  CONFLICT 79 79 I -> V (in Ref. 2).
FT  CONFLICT 644 644 S -> A (in Ref. 2).
SQ  SEQUENCE 657 AA; 73302 MW; 10D70CAB8E3E3AC CRC64;

Query Match 2.5%; Score 11; DB 1; Length 657;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 183 SEFILACQOMT 193
Db 396 SEFILACQOMT 406

RESULT 12
Q7QSR7_ANOGA PRELIMINARY; PRT; 677 AA.
AC Q7QSR7;
DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT 07-DEC-2004, sequence version 2.
DT 07-FEB-2006, entry version 10.
DE ENSANGP0000020538 (Fragment).
GN ORFNAMES=ENSANGG0000018049;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicidae;
OC Anophelinae; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RT "Anopheles gambiae re-annotation.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
DR EMBL; AAAB01008960; EAA10766.2; -; Genomic_DNA.
DR InterPro; IPR007603; DUF580.
DR PANTHER; PTHR12385; DUF580; 1.
DR Pfam; PF04515; DUF580; 1.
FT NON_TER 677 677
SQ SEQUENCE 677 AA; 76258 MW; 0EB24759D946739E CRC64;

Query Match 2.2%; Score 10; DB 2; Length 677;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 177 IGLIWTSEFI 186
Db 418 IGLIWTSEFI 427

RESULT 13
Q4H957_9DEIO PRELIMINARY; PRT; 155 AA.
AC Q4H957;
DT 16-AUG-2005, integrated into UniProtKB/TrEMBL.
DT 16-AUG-2005, sequence version 1.
DT 07-FEB-2006, entry version 2.
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CC -----
DE EMBL; AAAB01008960; EAA10766.2; -; Genomic_DNA.
DR InterPro; IPR007603; DUF580.
DR PANTHER; PTHR12385; DUF580; 1.
DR Pfam; PF04515; DUF580; 1.
FT NON_TER 677 677
SQ SEQUENCE 677 AA; 76258 MW; 0EB24759D946739E CRC64;
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DE Hypothetical protein precursor.
GN ORFNAMES=DgeodRAFT_1048;
OS Deinococcus geothermalis DSM 11300.
OC Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;
OC Deinococcaceae; Deinococcus.
OX NCBI_TaxID=319795;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DSM 11300;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Capellan A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.;
RT "Sequencing of the draft genome assembly of Deinococcus geothermalis
RT DSM 11300.";
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DSM 11300;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Deinococcus geothermalis
RT DSM 11300.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -----
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CC -----
DR EMBL; AAHE01000005; EAL82795.1; -; Genomic_DNA.
DR Hypothetical protein; Signal.
FT SIGNAL 1 35 Potential.
SQ SEQUENCE 155 AA; 16438 MW; 535B68D3C554DC35 CRC64;

Query Match 2.0%; Score 9; DB 2; Length 155;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 138 LWVAVLLSL 146
Db 18 LWVAVLLSL 26

RESULT 14
Q9A2U8_CAUCR PRELIMINARY; PRT; 263 AA.
ID Q9A2U8;
DT 01-JUN-2001, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2001, sequence version 1.
DT 07-FEB-2006, entry version 15.
DE Hypothetical protein CC3458.
GN OrderedLocusNames=CC3458;
OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
OC Caulobacteraceae; Caulobacter.
OX NCBI_TaxID=155892;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 19089 / CB15;
RX MEDLINE=21173698; PubMed=11259647; DOI=10.1073/pnas.061029298;
RA Eisen J.A., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
RA Kolonay J.F., Smit J., Craven M.B., Khouri H.M., Shetty J.,
RA Berry K.J., Utterback T.R., Tran K., Wolf A.M., Vamathevan J.J.,
RA Ermolaeva M.D., White O., Salzberg S.L., Venter J.C., Shapiro L.,
RA Fraser C.M.;
RT "Complete genome sequence of Caulobacter crescentus.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
CC -----
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CC -----
DR EMBL; AE006004; AAK25420.1; -; Genomic_DNA.
DR FIR; H87677; H87677.
DR TIGR; CC3458; -.
DR InterPro; IPR003675; Abi.
DR Pfam; PF02517; Abi; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 263 AA; 28189 MW; 1AFB12DDA9E9E1D8 CRC64;

Query Match          2.0%; Score 9; DB 2; Length 263;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 LALALSLAM 21
Db 95 LALALSLAM 103

RESULT 15
Q74K77_LACJO
ID Q74K77_LACJO PRELIMINARY; PRT; 77 AA.
AC Q74K77;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE Hypothetical protein.
GN OrderedLocusNames=LJ0876; ORFNames=LJ_0876;
OS Lactobacillus johnsonii.
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=33959;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=NCC 533;
RA PubMed=14983040; DOI=10.1073/pnas.0307327101;
RA Priddy R.D., Berger B., Desiere F., Vilanova D., Barretto C.,
RA Pittet A.-C., Zwahlen M.-C., Rouvet M., Altermann E., Barrangou R.,
RA Mollet B., Mercenier A., Kleenhammer T., Arigoni F., Schell M.A.;
RT "The genome sequence of the probiotic intestinal bacterium
RT Lactobacillus johnsonii NCC 533."
RL Proc. Natl. Acad. Sci. U.S.A. 101:2512-2517(2004).
CC -----
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CC -----
DR EMBL; AE017198; AAS08697.1; -; Genomic_DNA.
DR BioCyc; LJ0H257314:LJ0876-MONOMER; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0015450; F:protein translocase activity; IEA.
DR GO; GO:0009306; P:protein secretion; IEA.
DR InterPro; IPR004692; SecG.
DR Pfam; PF03840; SecG; 1.
DR PRINTS; PR01651; SECSEXPORT.
DR TIGRFAMs; TIGR00810; secG; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 77 AA; 8398 MW; C64B75955A84D18 CRC64;

Query Match          1.8%; Score 8; DB 2; Length 77;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86 ITAVLLVL 93
Db 56 ITAVLLVL 63

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Search completed: June 6, 2006, 22:29:22
Job time : 299 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 6, 2006, 22:24:36 ; Search time 41 Seconds
(without alignments)
1044.304 Million cell updates/sec

Title: US-10-063-537-32
Perfect score: 445
Sequence: 1 MGRDTILGLCILALSLA.....QQDKHLRNEEGTELOAIVR 445

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 6
Total number of hits satisfying chosen parameters: 2646

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR 80:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	9	2.0	263	2 H87677	conserved hypother
2	8	1.8	132	2 D82670	general secretory
3	8	1.8	288	2 A64123	cryptophan synthas
4	8	1.8	293	2 B83783	hypothetical prote
5	8	1.8	293	2 T27430	hypothetical prote
6	8	1.8	360	2 I53032	bone morphogenetic
7	8	1.8	472	1 BMHU3	bone morphogenetic
8	8	1.8	761	2 S66719	hypothetical prote
9	8	1.8	764	2 T43751	cytochrome-c oxida
10	8	1.8	962	2 D70861	probable membranep
11	8	1.8	1023	2 AE1280	ATP-dependent dsDN
12	8	1.8	1023	2 AE1643	ATP-dependent dsDN
13	8	1.8	1578	2 S76238	hypothetical prote
14	7	1.6	48	2 B64647	hypothetical prote
15	7	1.6	51	2 D81271	small hydrophobic
16	7	1.6	52	2 AD1716	hypothetical prote
17	7	1.6	89	2 A69833	hypothetical prote
18	7	1.6	93	2 S66290	alpha 1 antichymot
19	7	1.6	98	2 E90606	hypothetical prote
20	7	1.6	112	2 S75298	hypothetical prote
21	7	1.6	112	2 AE2244	hypothetical prote
22	7	1.6	143	2 C84118	hypothetical prote
23	7	1.6	146	2 H75394	conserved hypother
24	7	1.6	161	2 S04765	IAF52 protein prec
25	7	1.6	165	2 G72486	hypothetical prote
26	7	1.6	166	2 S60634	cytochrome-c oxida
27	7	1.6	166	2 S25600	cytochrome-c oxida
28	7	1.6	166	2 G75478	ribosomal protein
29	7	1.6	181	2 AH3518	hypothetical prote

30	7	1.6	185	2 D82828	dTDP-4-dehydroxam
31	7	1.6	185	2 G89895	conserved hypother
32	7	1.6	199	2 T26157	hypothetical prote
33	7	1.6	199	2 T19616	hypothetical prote
34	7	1.6	207	2 F64223	hypothetical prote
35	7	1.6	207	2 B75327	hypothetical prote
36	7	1.6	209	2 A90608	hypothetical prote
37	7	1.6	210	2 G72507	hypothetical prote
38	7	1.6	212	2 T12644	NADH2 dehydrogenas
39	7	1.6	215	2 E70102	S-adenosylmethioni
40	7	1.6	223	2 T35424	probable regulator
41	7	1.6	226	2 H83185	hypothetical prote
42	7	1.6	234	2 H98154	amino acid ABC tra
43	7	1.6	234	2 AD3133	hypothetical prote
44	7	1.6	247	2 AD0757	cobalamin (5'-phos
45	7	1.6	248	2 C90984	probable glycosyl

ALIGNMENTS

RESULT 1

H87677
conserved hypothetical protein CC3458 [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: H87677
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: H87677
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-263 <STO>
A;Cross-references: UNIPROT:Q9A2U8; UNIPARC:UPI00000C7AAB; GB:AE003673; NID:gl3425176; PJ
C;Genetics:
A;Gene: CC3458

Query Match 2.0%; Score 9; DB 2; Length 263;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	13	LALALS	21
DB	95	LALALS	103

RESULT 2

D82670
general secretory pathway protein I precursor XF1521 [imported] - Xylella fastidiosa (str:
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 05-Oct-2004
C;Accession: D82670
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A83515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: D82670
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-132 <SIM>
A;Cross-references: UNIPROT:Q9PD58; UNIPARC:UPI00000C2760; GB:AE003982; GB:AE003849; NID
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, P.A.; Acencio, M.; Alvarenga, R.; AJ
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carrato, D.M.; Carver, H
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohme
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigra

chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, B.
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, R.C.; Miyaki, C.Y.;
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, E.C.; Palmieri, D.A.
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
M.; Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silv
M.; Tuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A;Reference number: A59328
A;Contents: annotation
C;Genetics:
A;Gene: XF1521
C;Superfamily: general secretion pathway protein I precursor

Query Match 1.8%; Score 8; DB 2; Length 132;
Best Local Similarity 100.0%; Pred. No. 6; Mismatches 0; Indels 0; Gaps 0;
Matches 8; Conservative 0;

QY 12 ILALALS 19
Db 18 ILALALS 25
|||||

RESULT 3
A64123
tryptophan synthase (EC 4.2.1.20) alpha chain - Haemophilus influenzae (strain Rd KW20)
C;Species: Haemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
C;Accession: A64123
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J
; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M.
Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,
A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A;Reference number: A64000; MUID:95350630; PMID:7542800
A;Accession: A64123
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-268 <TIGR>
A;Cross-references: UNIPROT:P43759; UNIPARC:UPI00001374CE; GB:U32822; GB:I42023; NID:gl5
C;Genetics:
A;Gene: trpA
C;Function:
A;Description: catalyzes conversion of indoleglycerol phosphate and serine to tryptophan
A;Pathway: tryptophan biosynthesis
A;Note: cofactor pyridoxal phosphate
A;Note: last step in pathway
C;Superfamily: tryptophan synthase alpha chain; tryptophan synthase alpha chain homology
C;Keywords: carbon-oxygen lyase; hydro-lyase; tryptophan biosynthesis
F;18-247/Domain: tryptophan synthase alpha chain homology <TRPA>
F;49/Active site: Glu #status: predicted

Query Match 1.8%; Score 8; DB 2; Length 268;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 144 LSLGTAGA 151
Db 225 LSLGTAGA 232
|||||

RESULT 4
B83783
hypothetical protein BH1066 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: B83783
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: B83783
A;Status: preliminary
A;Molecule type: DNA

A;Residues: 1-293 <STO>
A;Cross-references: UNIPROT:Q9KDZ5; UNIPARC:UPI00000C3AA3; GB:AP001510; GB:BA000004; NID:
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH1066
C;Superfamily: maltose transport protein malG

Query Match 1.8%; Score 8; DB 2; Length 293;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 234 SFLISVVR 241
Db 74 SFLISVVR 81
|||||

RESULT 5
T27430
hypothetical protein Y79H2A.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T27430
R;Matthews, L.
submitted to the EMBL Data Library, September 1999
A;Reference number: Z20365
A;Accession: T27430
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-293 <WIL>
A;Cross-references: UNIPROT:Q9UIR9; UNIPARC:UPI000061335; EMBL:AL110501; NID:e1542357; I
A;Experimental source: clone Y79H2A
C;Genetics:
A;Gene: CESP.Y79H2A.2
A;Introns: 30/3; 50/1; 85/1; 112/3; 180/3; 223/3
C;Superfamily: Caenorhabditis elegans hypothetical protein Y79H2A.2

Query Match 1.8%; Score 8; DB 2; Length 293;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 35 IFISLVIL 42
Db 23 IFISLVIL 30
|||||

RESULT 6
I53032
bone morphogenetic protein 3 - rat (fragment)
C;Species: Rattus sp. (rat)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 16-Jul-1999
C;Accession: I53032
R;Chen, D.; Feng, J.Q.; Feng, M.; Harris, M.A.; Mahy, P.; Mundy, G.R.; Harris, S.E.
DNA Cell Biol. 14, 235-239, 1995
A;Title: Sequence and expression of bone morphogenetic protein 3 mRNA in prolonged cultu
A;Reference number: I53032; MUID:95186061; PMID:7880444
A;Accession: I53032
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-360 <RES>
A;Cross-references: UNIPARC:UPI0000170CBA; GB:S77492; NID:g957225; PIDN:AAB33725.1; PID:g
C;Superfamily: inhibin

Query Match 1.8%; Score 8; DB 2; Length 360;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 217 SLSILFF 224
Db 331 SLSILFF 338
|||||

RESULT 7
BMH03

bone morphogenetic protein 3 precursor - human
 N;Alternate names: osteogenin
 C;Species: Homo sapiens (man)
 C;Date: 16-Sep-1992 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
 C;Accession: D37278
 R;Wozney, J.M.; Rosen, V.; Celeste, A.J.; Mitsock, L.M.; Whitters, M.J.; Kriz, R.W.; Hew
 Science 242, 1528-1534, 1988
 A;Title: Novel regulators of bone formation: molecular clones and activities.
 F;23-345/Domain: propeptide #status predicted <PRO>
 A;Accession: D37278
 A;Molecule type: mRNA
 A;Residues: 1-472 <WQA>
 A;Cross-references: UNIPROT:P12645; UNIPARC:UPI0000126A25; GB:M22491; NID:G179505; PIDN:
 C;Genetics:
 A;Gene: GDB:BMP3
 A;Cross-references: GDB:125206; OMIM:112263
 A;Map position: 4p14-q21
 C;Superfamily: inhibin
 C;Keywords: bone; glycoprotein
 F;1-22/Domain: signal sequence #status predicted <SIG>
 F;23-345/Domain: propeptide #status predicted <PRO>
 F;346-472/Product: bone morphogenetic protein 3 #status predicted <MAT>
 F;117,141,175,220,463/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 1.8%; Score 8; DB 1; Length 472;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 217 SSLSILFF 224
 Db 443 SSLSILFF 450
 |||||

RESULT 8
 S66719
 hypothetical protein YOL036w - yeast (Saccharomyces cerevisiae)
 N;Alternate names: hypothetical protein O2105
 C;Species: Saccharomyces cerevisiae
 C;Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 09-Jul-2004
 C;Accession: S66719
 R;Habbig, B.; Hattenhorst, U.; Hollenbergh, C.P.; Ramezani Rad, M.
 submitted to the Protein Sequence Database, July 1996
 A;Reference number: S66703
 A;Accession: S66719
 A;Molecule type: DNA
 A;Residues: 1-761 <HAB>
 A;Cross-references: UNIPROT:Q08206; UNIPARC:UPI000006C3BA; EMBL:Z74779; NID:gl419828; PI
 A;Experimental source: strain S288C
 C;Genetics:
 A;Gene: MIPS:YOL036w
 A;Cross-references: SGD:S0005396
 A;Map position: 15L

Query Match 1.8%; Score 8; DB 2; Length 761;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 308 KILSKNSS 315
 Db 624 KILSKNSS 631
 |||||

RESULT 9
 T43751
 cytochrome-c oxidase (EC 1.9.3.1) chain 1/2 [similarity] - slime mold (Dictyostelium dis
 C;Species: Dictyostelium discoideum
 C;Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 09-Jul-2004
 C;Accession: T43751
 R;Ogawa, S.; Yoshino, R.; Angata, K.; Pi, M.; Iwamoto, M.; Kuroe, K.; Matsuo, K.; Morio,
 submitted to the EMBL Data Library, December 1996
 A;Description: The mitochondrial DNA of Dictyostelium discoideum. Complete sequence, gen
 A;Reference number: Z22666
 A;Accession: T43751

A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-764 <OGA>
 A;Cross-references: UNIPROT:O21042; UNIPARC:UPI0000090BE1; EMBL:AB000109; PIDN:BAA78055.1
 C;Genetics:
 A;Gene: cox1/2
 A;Genome: mitochondrion
 A;Introns: 89/2; 258/3; 387/3; 637/3
 C;Superfamily: Acanthamoeba cytochrome-c oxidase chain I/II; cytochrome-c oxidase chain
 C;Keywords: copper; electron transfer; heme; iron; magnesium; membrane-associated complex
 F;80,396/Binding site: heme a iron (His) (axial ligand) #status predicted
 F;259,308,309/Binding site: copper (His) #status predicted
 F;259-263/Cross-link: 1'-histidyl-3'-tyrosine (His-Tyr) #status predicted
 F;263/Binding site: oxygen (Tyr) #status predicted
 F;386,736/Binding site: magnesium (His, Glu) #status predicted
 F;394/Binding site: heme a3 iron (His) (axial ligand) #status predicted
 F;699,734,738,745/Binding site: copper 1 (His, Cys, Cys, Met) #status predicted
 F;734,736,738,742/Binding site: copper 2 (Cys, Glu, Cys, His) #status predicted

Query Match 1.8%; Score 8; DB 2; Length 764;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86 ITAVLLVL 93
 Db 209 ITAVLLVL 216
 |||||

RESULT 10
 D70661
 probable membrane protein with strong - Mycobacterium tuberculosis (strain H37RV)
 C;Species: Mycobacterium tuberculosis
 C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
 C;Accession: D70661
 R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.
 ; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.;
 Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
 Nature 393, 537-544, 1998
 A;Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
 A;Reference number: A70500; MUID:98295987; PMID:9634230
 A;Accession: D70661
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-962 <COL>
 A;Cross-references: UNIPROT:P95235; UNIPARC:UPI000012F275; GB:Z83860; GB:AL123456; NID:9-
 A;Experimental source: strain H37RV
 C;Genetics:
 A;Gene: mmpL9

Query Match 1.8%; Score 8; DB 2; Length 962;
 Best Local Similarity 100.0%; Pred. No. 32;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 142 VLLSLGTA 149
 Db 802 VLLSLGTA 809
 |||||

RESULT 11
 AE1280
 ATP-dependent dsDNA exonuclease SbcC homolog lmo1645 [imported] - Listeria monocytogenes
 C;Species: Listeria monocytogenes
 C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
 C;Accession: AE1280
 R;Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker,
 ; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
 D.; Jones, L.M.; Karst, U.
 Science 294, 849-852, 2001
 A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mat
 ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
 A;Title: Comparative genomics of Listeria species.
 A;Reference number: AB1077; MUID:21537279; PMID:11679669

A;Accession: AE1280
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1023 <GLA>
A;Cross-references: UNIPROT:Q9Y6N9; UNIPARC:UPI000005500D; GB:NC_003210; PIDN:CAC99723.1
A;Experimental source: strain EGD-e
C;Genetics:
A;Gene: lmo1645

Query Match 1.8%; Score 8; DB 2; Length 1023;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 LALALSIA 20
Db 935 LALALSIA 942
|||||

RESULT 12
AE1643
ATP-dependent dsDNA exonuclease SbcC homolog sbcC [imported] - *Listeria innocua* (strain
C;Species: *Listeria innocua*
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AE1643
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker
; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Krefit, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlant,
A;Title: Comparative Genomics of *Listeria* species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AE1643
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1023 <GLA>
A;Cross-references: UNIPROT:Q92B64; UNIPARC:UPI000000CC623; GB:AL592022; PIDN:CAC96917.1;
A;Experimental source: strain Clp11262
C;Genetics:
A;Gene: sbcC

Query Match 1.8%; Score 8; DB 2; Length 1023;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 LALALSIA 20
Db 935 LALALSIA 942
|||||

RESULT 13
S76238
hypotheical protein sil0267 - *Synechocystis* sp. (strain PCC 6803)
C;Species: *Synechocystis* sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S76238
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis*
s.
A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S76238
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-1578 <KAN>
A;Cross-references: UNIPROT:P74400; UNIPARC:UPI00000C10E9; EMBL:D90914; GB:AB001339; NID
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 1.8%; Score 8; DB 2; Length 1578;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 88 AVLLVLIIF 95
Db 23 AVLLVLIIF 30
|||||

RESULT 14

B64647
hypotheical protein HP1018 - *Helicobacter pylori* (strain 26695)

C;Species: *Helicobacter pylori*
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C;Accession: B64647

R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.;
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.
Nature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.N
A;Title: The complete genome sequence of the gastric pathogen *Helicobacter pylori*.
A;Reference number: A64520; MUID:97394467; PMID:9252185

A;Accession: B64647

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-48 <TOM>

A;Cross-references: UNIPROT:Q25662; UNIPARC:UPI00000C08DD; GB:AE000610; GB:AE000511; NID:

Query Match 1.6%; Score 7; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 LALALS 19
Db 9 LALALS 15
|||||

RESULT 15

DB1271

small hydrophobic protein Cj1728c [imported] - *Campylobacter jejuni* (strain NCTC 11168)
C;Species: *Campylobacter jejuni*
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004

C;Accession: DB1271

R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling

C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVleet, A.; Whitehead, S.; Barrell

Nature 403, 665-668, 2000

A;Title: The genome sequence of the food-borne pathogen *Campylobacter jejuni* reveals hyp

A;Reference number: AB1250; MUID:20150912; PMID:10688204

A;Accession: DB1271

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-51 <PAR>

A;Cross-references: UNIPROT:Q9PLV0; UNIPARC:UPI00000C1FEC; GB:AL139079; GB:AL111168; NID

A;Experimental source: serotype O2, strain NCTC 11168

C;Genetics:

A;Gene: Cj1728c

Query Match 1.6%; Score 7; DB 2; Length 51;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 SLVILGL 44
Db 19 SLVILGL 25
|||||

Search completed: June 6, 2006, 22:30:09

Job time : 44 secs

November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New).
Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 6, 2006, 22:17:36 ; Search time 16 Seconds
(without alignments)
321.656 Million cell updates/sec

Title: US-10-063-537-32

Perfect score: 2315

Sequence: 1 MSGRDTILGLCHIALALSLA.....QQDKSLRNEGTLOAIVR 445

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 58871 seqs, 11565156 residues

Total number of hits satisfying chosen parameters: 58871

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New*

- 1: /EMC_Celerra_SID33/ptodata/2/pubpaa/US09_NEW_PUB.pbp.*
- 2: /EMC_Celerra_SID33/ptodata/2/pubpaa/US06_NEW_PUB.pbp.*
- 3: /EMC_Celerra_SID33/ptodata/2/pubpaa/US07_NEW_PUB.pbp.*
- 4: /EMC_Celerra_SID33/ptodata/2/pubpaa/US08_NEW_PUB.pbp.*
- 5: /EMC_Celerra_SID33/ptodata/2/pubpaa/PCT_NEW_PUB.pbp.*
- 6: /EMC_Celerra_SID33/ptodata/2/pubpaa/US10_NEW_PUB.pbp.*
- 7: /EMC_Celerra_SID33/ptodata/2/pubpaa/US11_NEW_PUB.pbp.*
- 8: /EMC_Celerra_SID33/ptodata/2/pubpaa/US60_NEW_PUB.pbp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2315	100.0	445	6	US-10-196-749-148
2	2315	100.0	445	7	US-11-101-316-32
3	428	18.5	321	7	US-11-101-316-10
4	335.5	14.5	363	6	US-10-953-349-11171
5	326.5	14.1	353	6	US-10-953-349-11172
6	300.5	13.0	325	6	US-10-953-349-11173
7	222	9.6	366	6	US-10-953-349-17831
8	192.5	8.3	305	6	US-10-953-349-17832
9	187.5	8.1	281	6	US-10-953-349-17833
10	111	4.8	462	6	US-10-953-349-7915
11	111	4.8	482	6	US-10-953-349-7914
12	111	4.8	488	6	US-10-953-349-7913
13	97	4.2	691	6	US-10-511-937-2995
14	95.5	4.1	446	6	US-10-953-349-29132
15	95	4.1	426	6	US-10-953-349-2596
16	95	4.1	649	6	US-10-953-349-2595
17	95	4.1	667	6	US-10-953-349-2594
18	91	3.9	355	6	US-10-953-349-31241
19	90	3.9	352	6	US-10-953-349-31240
20	89.5	3.9	366	6	US-10-953-349-30070
21	89.5	3.9	376	6	US-10-953-349-30069
22	89.5	3.9	418	6	US-10-953-349-10300
23	89.5	3.9	425	6	US-10-953-349-30068
24	89.5	3.9	440	6	US-10-953-349-10299
25	89.5	3.9	475	6	US-10-953-349-10298

Sequence 24340, A
Sequence 9, Appli
Sequence 3, Appli
Sequence 11418, A
Sequence 22475, A
Sequence 11417, A
Sequence 11416, A
Sequence 27707, A
Sequence 27706, A
Sequence 27705, A
Sequence 4547, Ap
Sequence 4546, Ap
Sequence 4545, Ap
Sequence 48, Appl
Sequence 2761, Ap
Sequence 12434, A
Sequence 15450, A
Sequence 15449, A

ALIGNMENTS

RESULT 1
US-10-196-749-148
; Sequence 148, Application US/10196749
; Publication No. US20060094864A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430RIC340
; CURRENT APPLICATION NUMBER: US/10/196,749
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 148
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-196-749-148

Query Match 100.0%; Score 2315; DB 6; Length 445;
Best Local Similarity 100.0%; Pred. No. 1.5e-187;
Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSGRDILGCIILALALSAMMTFFRITTLVHIFISVLIGLLFVCGVLMWLYDYDN 60
DB 1 MSGRDILGCIILALALSAMMTFFRITTLVHIFISVLIGLLFVCGVLMWLYDYDN 60
QY 61 DLSIELDTERENMKCVLGFATVSTGITAVLLVLIIFVLRKRIKLTVELFOITNKAISSAPF 120
DB 61 DLSIELDTERENMKCVLGFATVSTGITAVLLVLIIFVLRKRIKLTVELFOITNKAISSAPF 120
QY 121 LFPQPLWTFAILIFFWVWVAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMSYHLIGLI 180
DB 121 LFPQPLWTFAILIFFWVWVAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMSYHLIGLI 180
QY 181 WTSEFILACQOMTIAGAVVTCYFNRSKNDDPPDHPILSSLSILFFYHOGTVVKGSLISVV 240
DB 181 WTSEFILACQOMTIAGAVVTCYFNRSKNDDPPDHPILSSLSILFFYHOGTVVKGSLISVV 240
QY 241 RIPRIIVMYMKNALKEQHGALSRYLFRCCYCCFWCLDKYLLHLNQNAVTTTAINGTDFC 300
DB 241 RIPRIIVMYMKNALKEQHGALSRYLFRCCYCCFWCLDKYLLHLNQNAVTTTAINGTDFC 300
QY 301 TSAKDAFKILSKNSHFTSINCFGDFIIFLGKVLVVCFTVFGGLMAFNYNRAFOQWAVPL 360
DB 301 TSAKDAFKILSKNSHFTSINCFGDFIIFLGKVLVVCFTVFGGLMAFNYNRAFOQWAVPL 360
QY 361 LLVAFAYLVAHSFSLVFETVLDALFLCPAVDLETNDGSEKPYFMDQEFSLFVKRSNKL 420
DB 361 LLVAFAYLVAHSFSLVFETVLDALFLCPAVDLETNDGSEKPYFMDQEFSLFVKRSNKL 420
QY 421 NNARAQDQKXSLRNEEGTELOAIVR 445
DB 421 NNARAQDQKXSLRNEEGTELOAIVR 445

RESULT 2
US-11-101-316-32
; Sequence 32, Application US/11101316
; Publication No. US20060099657A1
; GENERAL INFORMATION:
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: ANTIBODIES TO A POLYPEPTIDE ENCODED BY A NUCLEIC ACID
; FILE REFERENCE: P3230R1C17C1
; CURRENT APPLICATION NUMBER: US/11/101,316
; CURRENT FILING DATE: 2005-04-06
; PRIOR APPLICATION NUMBER: 10/063526
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: 10/006867
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 09/380137
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 32
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-101-316-32

Query Match 100.0%; Score 2315; DB 7; Length 445;

Best Local Similarity 100.0%; Pred. No. 1.5e-187;
Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSGRDILGCIILALALSAMMTFFRITTLVHIFISVLIGLLFVCGVLMWLYDYDN 60
DB 1 MSGRDILGCIILALALSAMMTFFRITTLVHIFISVLIGLLFVCGVLMWLYDYDN 60
QY 61 DLSIELDTERENMKCVLGFATVSTGITAVLLVLIIFVLRKRIKLTVELFOITNKAISSAPF 120
DB 61 DLSIELDTERENMKCVLGFATVSTGITAVLLVLIIFVLRKRIKLTVELFOITNKAISSAPF 120
QY 121 LFPQPLWTFAILIFFWVWVAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMSYHLIGLI 180
DB 121 LFPQPLWTFAILIFFWVWVAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMSYHLIGLI 180
QY 181 WTSEFILACQOMTIAGAVVTCYFNRSKNDDPPDHPILSSLSILFFYHOGTVVKGSLISVV 240
DB 181 WTSEFILACQOMTIAGAVVTCYFNRSKNDDPPDHPILSSLSILFFYHOGTVVKGSLISVV 240
QY 241 RIPRIIVMYMKNALKEQHGALSRYLFRCCYCCFWCLDKYLLHLNQNAVTTTAINGTDFC 300
DB 241 RIPRIIVMYMKNALKEQHGALSRYLFRCCYCCFWCLDKYLLHLNQNAVTTTAINGTDFC 300
QY 301 TSAKDAFKILSKNSHFTSINCFGDFIIFLGKVLVVCFTVFGGLMAFNYNRAFOQWAVPL 360
DB 301 TSAKDAFKILSKNSHFTSINCFGDFIIFLGKVLVVCFTVFGGLMAFNYNRAFOQWAVPL 360
QY 361 LLVAFAYLVAHSFSLVFETVLDALFLCPAVDLETNDGSEKPYFMDQEFSLFVKRSNKL 420
DB 361 LLVAFAYLVAHSFSLVFETVLDALFLCPAVDLETNDGSEKPYFMDQEFSLFVKRSNKL 420
QY 421 NNARAQDQKXSLRNEEGTELOAIVR 445
DB 421 NNARAQDQKXSLRNEEGTELOAIVR 445

RESULT 3
US-11-101-316-10
; Sequence 10, Application US/11101316
; Publication No. US20060099657A1
; GENERAL INFORMATION:
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: ANTIBODIES TO A POLYPEPTIDE ENCODED BY A NUCLEIC ACID
; FILE REFERENCE: P3230R1C17C1
; CURRENT APPLICATION NUMBER: US/11/101,316
; CURRENT FILING DATE: 2005-04-06
; PRIOR APPLICATION NUMBER: 10/063526
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: 10/006867
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 09/380137
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 10
; LENGTH: 321
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-101-316-10

Query Match 18.5%; Score 428; DB 7; Length 321;
Best Local Similarity 34.6%; Pred. No. 4e-29;
Matches 91; Conservative 55; Mismatches 93; Indels 24; Gaps 6;

```

QY 174 YHILGLIWTSEFILACQMTIAGAVTTCYFNRSK-NDPPDHPILSSLSILFFHQGTGVK 232
DB 56 YGVGLGLFWLNNWVLAQCGLAFASFYWAFHKQDIPTFPLISAFIRTLRYHTGSLAF 115
QY 233 GSFLISVVRIPRIIYVMONALKEQHGALSRYLFCRCYCCFWCLDKYLLHLNQNAYTTT 292
DB 116 GAILTLVQIARVILEYIDHKLGVQN-PVARCIMCCFKCLWCLEKFIKFLNRNAYIMI 174
QY 293 AINGTDFCTSAKDAFKILSKNSHFTSINCFDPIIFLGLKLVV-----CFTVFGGLMA 346
DB 175 AIYGNKFCVSAKNAFMLMENVVVVLDKVTDLFFGLLVGGVGLSFFFFSGRIP 234
QY 347 -----FNNRAPOQWAVPVLVAFAYLVVAFVLSVFTVLDALFCFAVDLETN 396
DB 235 GLGKDFKSPHLNY-----YV-LPIMTSLGAYVIASGFFSVFGMVCVDTLFCLFLEDLERN 288
QY 397 DGSSEKPYFMDQEFSLPVKESNK 419
DB 289 NGSUDRPYNSKSLKILGKNE 311

RESULT 4
US-10-953-349-11171
; Sequence 11171, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 11171
; LENGTH: 363
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-11171

Query Match 14.5%; Score 335.5; DB 6; Length 363;
Best Local Similarity 27.8%; Pred. No. 2.7e-21;
Matches 95; Conservative 63; Mismatches 137; Indels 47; Gaps 11;

QY 99 KRILKTVLQITNKAISSAPFLLFQPLWTFAILFPFWLVAVLLSLGTAGAAQVME-- 156
DB 7 RRLMATSVLKVAKVIGEVOALIIPAIPEFAMLAIFYMFWISAALHLFSSG--QVVQNN 64
QY 157 -----GGQVEYKPLSGIRYMWSYHLGLIWTSEFILACQMTI 194
DB 65 CNNTNCCAYDLVLKVNCDRCGYSIHYTPTHTIAIF--FHLFGCYWATQFFIASSATVI 122
QY 195 AGAVTTCYFNRSKNDP--PDHPILSSLSILFFHQGTGVKGSFLISVVRIPRIIYVMON 252
DB 123 AGSVASYWAQGEASPEIPFLPVFASMKRLARYNLGSLVSLVSFVESVRFLEAIRR 182
QY 253 ALK-----EQHGALSRYLFR--CCYCCFWCLDKYLLHLNQNAYTTTAINGTDFCTSAKD 305
DB 183 KTKVSGTIPDHFWRMAHYTSRGLCKSVETIKS-----VNRNAYIMAITGKSFCKSSAI 238
QY 306 AFKILSKNSHFTSINCFDPIIFLGLKLVVCFET--VFGGLM--AFNNYRAFOQWAVPVL- 361
DB 239 ATELIISNLRIGKVNVIQGVILFGLKLCVLSFALSALFGLMLDLSHRYRASHNKVSSPLP 298
QY 362 LVAFPA--YLVAFSFLSVFETVLDALFCFAVDLETDGSGS 401
DB 299 VLACWALGYIVATLFFAVVEMSIDTILSFQDSEENQGNQAQ 340

RESULT 5
US-10-953-349-11172
; Sequence 11172, Application US/10953349

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; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 11172
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-11172

Query Match 14.1%; Score 326.5; DB 6; Length 353;
Best Local Similarity 27.5%; Pred. No. 1.5e-20;
Matches 93; Conservative 62; Mismatches 136; Indels 47; Gaps 11;

QY 103 LTVLQITNKAISSAPFLLFQPLWTFAILFPFWLVAVLLSLGTAGAAQVME----- 156
DB 1 MATSVLKVAKVIGEVOALIIPAIPEFAMLAIFYMFWISAALHLFSSG--QVVQNNCNT 58
QY 157 -----GGQVEYKPLSGIRYMWSYHLGLIWTSEFILACQMTIAGAV 198
DB 59 NCCAYDLVLKVNCDRCGYSIHYTPTHTIAIF--FHLFGCYWATQFFIASSATVIAGSV 116
QY 199 VTCYFNRSKNDP--PDHPILSSLSILFFHQGTGVKGSFLISVVRIPRIIYVMONALK- 255
DB 117 ASYWAQGEASPEIPFLPVFASMKRLARYNLGSLVSLVSFVESVRFLEAIRRKT 176
QY 256 -----EQHGALSRYLFR--CCYCCFWCLDKYLLHLNQNAYTTTAINGTDFCTSAKDAFKI 309
DB 177 SGTIPDHFWRMAHYTSRGLCKSVETIKS-----VNRNAYIMAITGKSFCKSSAIATEL 232
QY 310 LSKNSHFTSINCFDPIIFLGLKLVVCFET--VFGGLM--AFNNYRAFOQWAVPVL-LVAF 365
DB 233 IISNLRIGKVNVIQGVILFGLKLCVLSFALSALFGLMLDLSHRYRASHNKVSSPLPVLAC 292
QY 366 FA--YLVAFSFLSVFETVLDALFCFAVDLETDGSGS 401
DB 293 WALGYIVATLFFAVVEMSIDTILSFQDSEENQGNQAQ 330

RESULT 6
US-10-953-349-11173
; Sequence 11173, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 11173
; LENGTH: 325
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-11173

Query Match 13.0%; Score 300.5; DB 6; Length 325;
Best Local Similarity 28.1%; Pred. No. 2.1e-18;
Matches 87; Conservative 57; Mismatches 119; Indels 47; Gaps 11;

QY 131 ILIFFFWLVAVLLSLGTAGAAQVME-----GGQVEYKPLS 166
DB 1 MLAIIFYMFWISAALHLFSSG--QVVQNNCNTNCCAYDLVLKVNCDRCGYSIHYTPHI 58
QY 167 GIRYMWSYHLGLIWTSEFILACQMTIAGAVTTCYFNRSKNDP--PDHFISSLSILFF 224

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GenCore version 5.1.9

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OM protein - protein search, using sw model

Run on: June 8, 2006, 23:59:01 ; Search time 186 Seconds
(without alignments)
1108.229 Million cell updates/sec

Perfect score: 2315

Sequence: 1 MSGRDTILGICILALSLA.....QQDKSLRNEEGTELQAIYR 445

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database : Published Applications AA Main:

- 1: /EMC_Celerra_SID33/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /EMC_Celerra_SID33/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 3: /EMC_Celerra_SID33/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 4: /EMC_Celerra_SID33/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 5: /EMC_Celerra_SID33/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 6: /EMC_Celerra_SID33/ptodata/2/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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27	2315	100.0	445	3	US-09-997-428-177
562	2315	100.0	445	4	US-10-174-587-148
626	2315	100.0	445	4	US-10-063-742-32
741	2315	100.0	445	5	US-10-972-317-32
743	2315	100.0	445	5	US-10-950-374-177
751	2315	100.0	445	6	US-11-102-240-32
752	2315	100.0	445	6	US-11-103-195-32
753	2314	99.9	653	4	US-10-062-937B-5
754	2314	99.9	653	4	US-10-391-399-73
755	2280.5	98.5	648	5	US-10-330-773-825
756	1696.5	73.3	558	5	US-10-330-773-822
757	1456	62.9	275	3	US-09-833-245-1911
758	1456	62.9	275	6	US-11-264-096-1911
759	1443	62.3	275	3	US-09-833-245-1910
760	1443	62.3	275	6	US-11-264-096-1910
761	1132	48.9	653	4	US-10-062-937B-9
762	1132	48.9	653	4	US-10-391-399-77
763	1121	48.4	654	4	US-10-062-937B-7
764	1121	48.4	654	4	US-10-391-399-75
765	1121	48.4	657	4	US-10-176-847-48
766	1121	48.4	657	5	US-10-753-267-6
767	1121	48.4	657	6	US-11-080-991-48
768	1121	48.4	708	4	US-10-106-698-6390
769	1116	48.2	646	4	US-10-062-937B-10
770	1116	48.2	646	4	US-10-391-399-78
771	1107	47.8	446	3	US-09-726-643-58
772	1107	47.8	446	4	US-10-042-141-58
773	1107	47.8	446	5	US-10-919-272-58

774	1107	47.8	510	3	US-09-726-643-139	Sequence 139, App
775	1107	47.8	510	4	US-10-042-141-139	Sequence 139, App
776	1107	47.8	510	5	US-10-919-272-139	Sequence 139, App
777	789.5	34.1	601	5	US-10-745-586-174	Sequence 174, App
778	624.5	27.0	691	6	US-11-097-143-831	Sequence 831, App
779	594.5	25.7	704	4	US-10-285-045-7	Sequence 7, Appli
780	594.5	25.7	704	4	US-10-284-660-7	Sequence 7, Appli
781	594.5	25.7	704	5	US-10-807-635-7	Sequence 7, Appli
782	594.5	25.7	704	5	US-10-936-138-7	Sequence 7, Appli
783	593.5	25.6	695	4	US-10-139-496-4	Sequence 4, Appli
784	590.5	25.5	704	4	US-10-468-334-1	Sequence 1, Appli
785	589.5	25.5	706	4	US-10-062-937B-8	Sequence 8, Appli
786	589.5	25.5	706	4	US-10-139-496-2	Sequence 2, Appli
787	589.5	25.5	706	4	US-10-322-774-7	Sequence 7, Appli
788	589.5	25.5	706	4	US-10-391-399-76	Sequence 76, Appli
789	587	25.4	706	5	US-10-789-378-26	Sequence 26, Appli
790	577.5	24.9	696	5	US-10-417-375-86	Sequence 86, Appli
791	577.5	24.9	696	5	US-10-417-375-90	Sequence 90, Appli
792	577.5	24.9	698	5	US-10-417-375-84	Sequence 84, Appli
793	577.5	24.9	698	5	US-10-417-375-88	Sequence 88, Appli
794	576.5	24.9	690	4	US-10-210-172-24	Sequence 24, Appli
795	568	24.5	717	4	US-10-062-937B-2	Sequence 2, Appli
796	568	24.5	717	4	US-10-391-399-70	Sequence 70, Appli
797	568	24.5	717	4	US-10-768-158-26	Sequence 26, Appli
798	563	24.3	717	4	US-10-104-047-3465	Sequence 3465, Ap
799	563	24.3	717	6	US-11-072-512-3465	Sequence 3465, Ap
800	561.5	24.3	585	4	US-10-276-774-1968	Sequence 1968, Ap
801	552	23.8	453	3	US-09-833-245-713	Sequence 713, App
802	552	23.8	453	6	US-11-264-096-713	Sequence 713, App
803	551	23.8	804	5	US-10-417-375-81	Sequence 81, Appli
804	543	23.5	453	3	US-09-833-245-712	Sequence 712, App
805	543	23.5	453	6	US-11-264-096-712	Sequence 712, App
806	543	23.5	456	4	US-10-264-049-2982	Sequence 2982, Ap
807	540	23.3	710	4	US-10-285-045-2	Sequence 2, Appli
808	540	23.3	710	4	US-10-284-660-2	Sequence 2, Appli
809	540	23.3	710	4	US-10-306-631-3	Sequence 3, Appli
810	540	23.3	710	4	US-10-306-631-5	Sequence 5, Appli
811	540	23.3	710	4	US-10-306-631-7	Sequence 7, Appli
812	540	23.3	710	4	US-10-306-631-9	Sequence 9, Appli
813	540	23.3	710	4	US-10-306-631-13	Sequence 13, Appli
814	540	23.3	710	4	US-10-306-631-20	Sequence 20, Appli
815	540	23.3	710	4	US-10-306-631-21	Sequence 21, Appli
816	540	23.3	710	4	US-10-306-631-23	Sequence 23, Appli
817	540	23.3	710	4	US-10-306-631-27	Sequence 27, Appli
818	540	23.3	710	4	US-10-306-631-75	Sequence 75, Appli
819	540	23.3	710	4	US-10-306-631-98	Sequence 98, Appli
820	540	23.3	710	4	US-10-306-631-104	Sequence 104, App
821	540	23.3	710	4	US-10-306-631-110	Sequence 110, App
822	540	23.3	710	4	US-10-306-631-112	Sequence 112, App
823	540	23.3	710	5	US-10-807-635-2	Sequence 2, Appli
824	539	23.3	710	5	US-10-936-138-2	Sequence 2, Appli
825	539	23.3	710	4	US-10-168-651-22	Sequence 22, Appli
826	539	23.3	710	4	US-10-306-631-11	Sequence 11, Appli
827	539	23.3	710	4	US-10-306-631-22	Sequence 22, Appli
828	539	23.3	710	4	US-10-306-631-28	Sequence 28, Appli
829	538.5	23.3	705	4	US-10-285-045-5	Sequence 5, Appli
830	538.5	23.3	705	5	US-10-284-660-5	Sequence 5, Appli
831	538.5	23.3	705	5	US-10-807-635-5	Sequence 5, Appli
832	538.5	23.3	705	5	US-10-936-138-5	Sequence 5, Appli
833	532	23.0	712	4	US-10-306-631-19	Sequence 19, Appli
834	532	23.0	712	4	US-10-306-631-26	Sequence 26, Appli
835	532	23.0	712	4	US-10-306-631-109	Sequence 109, App
836	532	23.0	712	4	US-10-306-631-111	Sequence 111, App
837	531	22.9	712	4	US-10-295-027-1369	Sequence 1369, Ap
838	524	22.6	722	4	US-10-306-631-17	Sequence 17, Appli
839	524	22.6	722	4	US-10-306-631-25	Sequence 25, Appli
840	524	22.6	722	4	US-10-306-631-103	Sequence 103, App
841	524	22.6	722	4	US-10-306-631-105	Sequence 105, App
842	517	22.3	403	6	US-10-104-047-2454	Sequence 2454, Ap
843	517	22.3	403	6	US-11-072-512-2454	Sequence 2454, Ap
844	513	22.2	796	6	US-11-097-143-35229	Sequence 35229, A
845	462	20.0	373	4	US-10-114-893-204	Sequence 204, App
846	460.5	19.9	626	4	US-10-425-114-71114	Sequence 71114, A

847	453.5	19.6	623	4	US-10-425-115-193134	Sequence 193134,	1139	108	4.7	474	4	US-10-282-122A-63555	Sequence 63555, A
848	452	19.5	598	4	US-10-306-631-15	Sequence 15, Appl	1140	108	4.7	1783	6	US-11-126-313-38	Sequence 38, Appl
849	452	19.5	598	4	US-10-306-631-24	Sequence 24, Appl	1141	108	4.7	1917	4	US-10-369-493-6036	Sequence 6036, Ap
850	452	19.5	598	4	US-10-306-631-97	Sequence 97, Appl	1142	107	4.6	345	4	US-10-359-285-5	Sequence 5, Appl1
851	452	19.5	598	4	US-10-306-631-99	Sequence 99, Appl	1143	106	4.6	489	4	US-10-017-161-716	Sequence 716, App
852	447	19.3	94	4	US-10-425-115-280712	Sequence 280712,	1144	106	4.6	497	5	US-10-646-132-1	Sequence 1, Appl1
853	447	19.3	38444	5	US-10-450-763-38444	Sequence 38444, A	1145	106	4.6	677	6	US-11-010-239-48	Sequence 48, Appl
854	428	18.5	288	4	US-10-364-237-2368	Sequence 2368, Ap	1146	104.5	4.5	352	5	US-10-739-930-10950	Sequence 10950, A
881	428	18.5	321	3	US-09-997-428-36	Sequence 36, Appl	1147	104.5	4.5	475	4	US-10-282-122A-64199	Sequence 64199, A
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1075	428	18.5	321	5	US-10-972-317-10	Sequence 10, Appl	1149	104	4.5	353	3	US-09-911-345-2	Sequence 2, Appl1
1076	428	18.5	321	6	US-10-950-374-36	Sequence 36, Appl	1150	104	4.5	353	4	US-10-032-697-2	Sequence 2, Appl1
1078	428	18.5	321	6	US-11-102-240-10	Sequence 10, Appl	1151	104	4.5	353	4	US-10-311-196-1	Sequence 1, Appl1
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1082	385.5	16.7	700	4	US-10-424-599-239983	Sequence 239983,	1155	103	4.4	234	4	US-10-001-857-176	Sequence 176, App
1083	382	16.5	711	4	US-10-437-963-117479	Sequence 117479,	1156	103	4.4	461	4	US-10-811-199-1	Sequence 1, Appl1
1084	381	16.5	678	4	US-10-437-963-117477	Sequence 117477,	1157	103	4.4	461	4	US-10-811-199-6	Sequence 6, Appl1
1085	376	16.2	598	4	US-10-425-114-38077	Sequence 38077, A	1158	103	4.4	465	3	US-09-915-181A-8	Sequence 8, Appl1
1086	376	16.2	705	4	US-10-425-115-358156	Sequence 358156,	1159	103	4.4	518	3	US-09-962-290-8	Sequence 8, Appl1
1087	370	16.0	184	3	US-09-925-300-956	Sequence 956, App	1160	103	4.4	663	4	US-10-425-114-65041	Sequence 65041, A
1088	366	15.8	719	4	US-10-437-963-117476	Sequence 117476,	1161	103	4.4	1080	6	US-11-096-568A-27723	Sequence 27723, A
1089	341	14.7	279	5	US-10-450-763-45993	Sequence 45993, A	1162	103	4.4	1097	6	US-11-096-568A-27722	Sequence 27722, A
1090	340	14.7	342	4	US-10-425-114-55911	Sequence 55911, A	1163	103	4.4	1128	6	US-11-096-568A-27721	Sequence 27721, A
1091	270	11.7	116	4	US-10-264-237-25246	Sequence 2546, Ap	1164	102.5	4.4	252	4	US-10-282-122A-62194	Sequence 62194, A
1092	230	9.9	329	3	US-09-864-761-45244	Sequence 45244, A	1165	102.5	4.4	389	6	US-11-188-298-18838	Sequence 18838, A
1093	228	9.8	329	4	US-10-420-120-317	Sequence 317, App	1166	102.5	4.4	395	2	US-08-900-230-5	Sequence 5, Appl1
1094	224.5	9.7	252	4	US-10-424-599-268532	Sequence 268532,	1167	102	4.4	378	4	US-10-164-649-5	Sequence 5, Appl1
1095	187.5	8.1	285	4	US-10-424-599-161447	Sequence 161447,	1168	102	4.4	383	4	US-10-225-567A-543	Sequence 543, App
1096	186	8.0	493	4	US-10-437-963-172685	Sequence 172685,	1169	102	4.4	446	3	US-09-826-509-487	Sequence 487, App
1097	181	7.8	518	4	US-10-032-585-7864	Sequence 7864, Ap	1170	102	4.4	446	4	US-10-277-078-4	Sequence 4, Appl
1098	172	7.4	46	4	US-10-425-115-336095	Sequence 336095,	1171	102	4.4	446	4	US-10-225-567A-98	Sequence 98, Appl
1099	164.5	7.1	193	4	US-10-767-701-52363	Sequence 52363, A	1172	102	4.4	446	4	US-10-299-642-2	Sequence 2, Appl1
1100	162.5	7.0	400	4	US-10-437-963-117475	Sequence 117475,	1173	102	4.4	446	4	US-10-299-642-4	Sequence 4, Appl1
1101	161.5	7.0	148	3	US-09-303-190-166	Sequence 166, App	1174	102	4.4	446	4	US-10-299-642-6	Sequence 6, Appl1
1102	161.5	7.0	148	3	US-09-978-360A-797	Sequence 797, App	1175	102	4.4	446	4	US-10-299-642-16	Sequence 16, Appl
1103	161.5	7.0	148	3	US-09-978-360A-797	Sequence 797, App	1176	102	4.4	446	4	US-10-292-798-628	Sequence 628, App
1104	161.5	7.0	148	5	US-10-930-331-166	Sequence 166, App	1177	102	4.4	446	5	US-10-925-095-487	Sequence 487, App
1105	149	6.4	284	4	US-10-424-599-244981	Sequence 244981,	1178	102	4.4	446	6	US-11-166-412-67	Sequence 67, Appl
1106	148.5	6.4	587	4	US-10-437-963-136252	Sequence 136252,	1179	102	4.4	495	5	US-09-776-865-4	Sequence 4, Appl1
1107	140	6.0	395	4	US-10-425-115-345164	Sequence 345164,	1180	102	4.4	636	4	US-10-823-506-4	Sequence 4, Appl1
1108	134	5.8	240	4	US-10-424-599-253590	Sequence 253590,	1181	102	4.4	434	4	US-10-425-115-289578	Sequence 289578,
1109	124	5.4	130	4	US-10-425-115-296800	Sequence 296800,	1182	101.5	4.4	347	4	US-10-254-905-9	Sequence 9, Appl1
1110	119	5.1	858	5	US-10-470-048B-333	Sequence 333, App	1183	101.5	4.4	348	3	US-09-966-782A-9	Sequence 9, Appl1
1111	114.5	4.9	603	6	US-11-097-143-4161	Sequence 4161, Ap	1184	101	4.4	357	4	US-10-017-161-2110	Sequence 2110, Ap
1112	113.5	4.9	186	4	US-10-425-115-225888	Sequence 225888,	1185	101	4.4	518	4	US-10-292-798-1756	Sequence 1756, Ap
1113	112.5	4.9	347	4	US-10-262-313-10	Sequence 10, Appl	1186	101	4.4	741	5	US-10-128-558-133	Sequence 133, App
1114	112.5	4.9	347	4	US-10-768-878-10	Sequence 10, Appl	1187	101	4.4	518	5	US-10-732-923-22026	Sequence 22026, A
1115	112.5	4.9	348	3	US-09-992-331-10	Sequence 2, Appl1	1188	100.5	4.3	292	4	US-10-437-963-182050	Sequence 182050,
1116	112.5	4.9	348	4	US-10-090-569-2	Sequence 5, Appl1	1189	100.5	4.3	335	4	US-10-017-161-448	Sequence 448, App
1117	112.5	4.9	348	4	US-10-212-980-5	Sequence 5, Appl1	1190	100.5	4.3	335	4	US-10-343-650A-626	Sequence 626, App
1118	112.5	4.9	348	4	US-10-081-810-54	Sequence 54, Appl	1191	100.5	4.3	373	4	US-10-137-731-2	Sequence 2, Appl1
1119	112.5	4.9	348	4	US-10-278-087A-46	Sequence 46, Appl	1192	100.5	4.3	373	4	US-10-228-667-2	Sequence 2, Appl1
1120	111.5	4.8	339	4	US-10-087-192-1467	Sequence 1467, Ap	1193	100.5	4.3	373	5	US-10-145-586-28	Sequence 28, Appl
1121	111.5	4.8	415	4	US-10-017-161-2412	Sequence 2412, Ap	1194	100.5	4.3	373	5	US-10-935-190-16	Sequence 16, Appl
1122	109.5	4.7	834	4	US-10-017-161-1996	Sequence 1996, Ap	1195	100.5	4.3	373	5	US-10-237-813-4	Sequence 4, Appl1
1123	108.5	4.7	345	4	US-10-262-313-11	Sequence 11, Appl	1196	100.5	4.3	611	5	US-10-505-486-67	Sequence 67, Appl
1124	108.5	4.7	345	4	US-10-254-905-10	Sequence 10, Appl	1197	100.5	4.3	862	6	US-11-097-143-5382	Sequence 5382, Ap
1125	108.5	4.7	346	4	US-10-768-878-11	Sequence 11, Appl	1198	100	4.3	391	4	US-10-282-122A-48531	Sequence 48531, A
1126	108.5	4.7	346	2	US-08-999-112-32	Sequence 32, Appl	1199	100	4.3	403	4	US-10-282-122A-49552	Sequence 49552, A
1127	108.5	4.7	346	3	US-09-966-782A-10	Sequence 10, Appl	1200	100	4.3	490	6	US-11-079-463-5351	Sequence 5351, Ap
1128	108.5	4.7	346	3	US-09-992-331-11	Sequence 11, Appl	1201	99.5	4.3	371	4	US-09-905-253A-4	Sequence 4, Appl1
1129	108.5	4.7	346	3	US-09-825-751A-83	Sequence 83, Appl	1202	99.5	4.3	371	4	US-10-201-187-4	Sequence 4, Appl1
1130	108.5	4.7	346	3	US-09-771-287-5	Sequence 5, Appl1	1203	99.5	4.3	371	5	US-10-603-566-4	Sequence 4, Appl1
1131	108.5	4.7	346	4	US-10-212-980-6	Sequence 6, Appl1	1204	99.5	4.3	371	5	US-10-893-485-4	Sequence 4, Appl1
1132	108.5	4.7	346	4	US-10-007-132-5	Sequence 5, Appl1	1205	99.5	4.3	371	5	US-10-237-813-5	Sequence 5, Appl1
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1134	108.5	4.7	346	4	US-10-298-992-7	Sequence 7, Appl1	1207	99.5	4.3	371	6	US-11-218-281-2	Sequence 2, Appl1
1135	108.5	4.7	346	4	US-10-285-019-30	Sequence 30, Appl	1208	99.5	4.3	371	6	US-11-218-281-33	Sequence 33, Appl
1136	108.5	4.7	346	4	US-10-466-205-1	Sequence 1, Appl1	1209	99	4.3	342	6	US-11-098-686-10521	Sequence 10521, A
1137	108.5	4.7	346	4	US-10-240-801A-11	Sequence 11, Appl	1210	99	4.3	371	4	US-09-905-253A-2	Sequence 2, Appl1
1138	108.5	4.7	346	5	US-10-851-438-83	Sequence 83, Appl	1211	99	4.3	371	4	US-10-201-187-2	Sequence 2, Appl1

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1213	99	4.3	371	4	US-10-282-798-664	Sequence 664, App	1286	96.5	4.2	953	4	US-10-128-714-3297	Sequence 3297, Ap
1214	99	4.3	371	4	US-10-603-566-2	Sequence 2, Appl	1287	96.5	4.2	954	4	US-10-437-963-204079	Sequence 204079, S
1215	99	4.3	371	5	US-10-753-267-128	Sequence 128, App	1288	96.5	4.2	1056	4	US-10-128-714-8297	Sequence 8297, Ap
1216	99	4.3	371	5	US-10-893-485-2	Sequence 2, Appl	1289	96	4.1	244	4	US-10-437-963-153664	Sequence 153664, S
1217	99	4.3	371	6	US-10-237-813-3	Sequence 3, Appl	1290	96	4.1	338	4	US-10-343-650A-678	Sequence 678, App
1218	99	4.3	371	6	US-11-134-811-2	Sequence 2, Appl	1291	96	4.1	416	4	US-10-335-977-5911	Sequence 5911, Ap
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1222	99	4.3	611	5	US-10-505-486-90	Sequence 90, Appl	1295	96	4.1	786	4	US-10-424-599-254383	Sequence 254383, S
1223	99	4.3	788	4	US-10-322-281-663	Sequence 663, App	1296	96	4.1	2288	4	US-10-736-883-40	Sequence 40, Appl
1224	98.5	4.3	394	4	US-10-282-122A-78100	Sequence 78100, A	1297	95.5	4.1	393	4	US-10-282-122A-43114	Sequence 43114, A
1225	98.5	4.3	442	4	US-10-282-122A-58720	Sequence 58720, A	1298	95	4.1	232	4	US-10-276-774-1924	Sequence 1924, Ap
1226	98.5	4.3	485	4	US-10-369-493-18121	Sequence 18121, A	1299	95	4.1	308	4	US-10-017-161-692	Sequence 692, App
1227	98.5	4.3	485	5	US-10-732-923-23457	Sequence 23457, A	1300	95	4.1	318	5	US-10-793-626-3118	Sequence 3118, Ap
1228	98.5	4.3	496	6	US-11-097-143-11013	Sequence 11013, A	1301	95	4.1	319	4	US-10-231-079-21	Sequence 21, Appl
1229	98.5	4.3	695	4	US-10-042-865-138	Sequence 138, App	1302	95	4.1	319	4	US-10-292-798-604	Sequence 604, App
1230	98.5	4.3	695	4	US-10-072-012-397	Sequence 397, App	1303	95	4.1	319	4	US-10-311-196-10	Sequence 10, Appl
1231	98	4.2	318	3	US-09-800-274-6	Sequence 6, Appl	1304	95	4.1	319	5	US-10-511-538-21	Sequence 21, Appl
1232	98	4.2	318	4	US-10-252-798-1732	Sequence 1732, Ap	1305	95	4.1	484	6	US-11-188-298-18146	Sequence 18146, A
1233	98	4.2	318	4	US-10-724-208-4	Sequence 4, Appl	1310	94.5	4.1	437	6	US-11-079-463-8067	Sequence 8067, Ap
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1235	98	4.2	321	5	US-10-724-209-4	Sequence 4, Appl	1312	94.5	4.1	701	5	US-10-437-963-162148	Sequence 162148, S
1236	98	4.2	321	5	US-10-986-871-4	Sequence 4, Appl	1313	94.5	4.1	735	4	US-10-437-963-162148	Sequence 162148, S
1237	98	4.2	321	5	US-10-017-161-2086	Sequence 2086, Ap	1314	94.5	4.1	741	5	US-10-450-763-55419	Sequence 55419, A
1238	98	4.2	338	4	US-10-017-161-2140	Sequence 2140, Ap	1315	94.5	4.1	857	6	US-11-052-554A-218	Sequence 218, App
1239	98	4.2	338	4	US-10-292-798-1786	Sequence 1786, Ap	1316	94	4.1	49	4	US-10-062-937B-12	Sequence 12, Appl
1240	98	4.2	338	4	US-10-343-650A-676	Sequence 676, App	1317	94	4.1	49	4	US-10-391-399-80	Sequence 80, Appl
1241	98	4.2	451	5	US-10-617-320-4466	Sequence 4466, Ap	1318	94	4.1	335	4	US-10-333-946-11	Sequence 11, Appl
1242	98	4.2	486	4	US-10-724-972A-4076	Sequence 4076, Ap	1319	94	4.1	340	3	US-09-791-932-117	Sequence 117, App
1243	98	4.2	642	4	US-10-282-122A-51332	Sequence 51332, A	1320	94	4.1	340	3	US-09-990-940-2	Sequence 2, Appl
1244	98	4.2	663	3	US-09-815-242-10070	Sequence 10070, A	1321	94	4.1	340	3	US-09-564-923A-2	Sequence 2, Appl
1245	98	4.2	663	4	US-10-287-274-332	Sequence 332, App	1322	94	4.1	340	4	US-10-225-567A-666	Sequence 666, App
1246	98	4.2	663	4	US-10-282-122A-56452	Sequence 56452, A	1323	94	4.1	340	4	US-10-291-990-29	Sequence 29, Appl
1247	97.5	4.2	250	4	US-10-282-122A-62825	Sequence 62825, A	1324	94	4.1	340	4	US-10-321-807-40	Sequence 40, Appl
1248	97.5	4.2	250	4	US-10-282-122A-64530	Sequence 64530, A	1325	94	4.1	340	4	US-10-332-082-3	Sequence 3, Appl
1249	97.5	4.2	250	4	US-10-225-567A-402	Sequence 402, App	1326	94	4.1	340	4	US-10-472-629-3	Sequence 3, Appl
1250	97.5	4.2	373	4	US-10-242-499-3	Sequence 3, Appl	1327	94	4.1	340	4	US-10-478-534-4	Sequence 4, Appl
1251	97.5	4.2	453	5	US-10-793-626-1516	Sequence 1516, App	1328	94	4.1	340	4	US-10-321-807-40	Sequence 40, Appl
1252	97.5	4.2	454	4	US-10-335-977-6163	Sequence 6163, Ap	1329	94	4.1	340	4	US-10-314-048A-40	Sequence 40, Appl
1253	97.5	4.2	456	4	US-10-335-977-6164	Sequence 6164, Ap	1330	94	4.1	340	4	US-10-477-985-58	Sequence 58, Appl
1254	97.5	4.2	512	3	US-09-962-290-2	Sequence 2, Appl	1331	94	4.1	340	4	US-10-680-402-2	Sequence 2, Appl
1255	97.5	4.2	512	3	US-10-282-122A-78152	Sequence 78152, A	1332	94	4.1	340	5	US-10-897-815-40	Sequence 40, Appl
1256	97.5	4.2	663	4	US-10-278-455-4	Sequence 4, Appl	1333	94	4.1	340	5	US-10-500-672-37	Sequence 37, Appl
1257	97.5	4.2	335	4	US-10-278-437-4	Sequence 4, Appl	1334	94	4.1	340	5	US-10-941-486-5	Sequence 5, Appl
1258	97.5	4.2	335	4	US-10-240-540-16	Sequence 16, Appl	1335	94	4.1	340	5	US-10-930-662-40	Sequence 40, Appl
1259	97.5	4.2	335	5	US-10-975-367-16	Sequence 16, Appl	1336	94	4.1	340	5	US-10-980-388-117	Sequence 117, App
1260	97.5	4.2	335	5	US-10-511-549-4	Sequence 4, Appl	1337	94	4.1	340	6	US-11-038-360-2	Sequence 2, Appl
1261	97.5	4.2	343	3	US-09-886-055-411	Sequence 411, App	1338	94	4.1	474	4	US-11-127-877-53	Sequence 53, Appl
1262	97.5	4.2	343	3	US-09-804-291-411	Sequence 411, App	1339	94	4.1	494	6	US-10-437-963-175542	Sequence 175542, S
1263	97.5	4.2	343	4	US-10-343-650A-496	Sequence 496, App	1340	94	4.1	495	3	US-11-079-463-8915	Sequence 8915, Ap
1264	97.5	4.2	343	4	US-10-467-252-13	Sequence 13, Appl	1341	94	4.1	495	3	US-09-915-181A-7	Sequence 7, Appl
1265	97.5	4.2	343	5	US-10-819-316-411	Sequence 411, App	1342	94	4.1	495	4	US-10-755-889-588	Sequence 588, App
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1270	97.5	4.2	613	4	US-10-225-567A-356	Sequence 356, App	1347	94	4.1	536	3	US-09-776-865-2	Sequence 2, Appl
1271	97.5	4.2	663	3	US-09-781-880-5	Sequence 5, Appl	1348	94	4.1	536	5	US-10-823-506-8	Sequence 8, Appl
1272	97.5	4.2	663	4	US-10-466-720-2	Sequence 2, Appl	1349	93.5	4.0	569	4	US-10-282-122A-75619	Sequence 75619, A
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1362	93	4.0	335	4	US-10-278-455-25	Sequence 25, Appl	1435	91	3.9	419	3	US-09-826-508-34	Sequence 34, Appl
1363	93	4.0	335	4	US-10-278-437-25	Sequence 25, Appl	1436	91	3.9	419	3	US-09-875-076-2	Sequence 2, Appl
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1365	93	4.0	356	4	US-10-447-328-82	Sequence 82, Appl	1438	91	3.9	419	3	US-09-811-838-8	Sequence 8, Appl
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OM protein - protein search, using sw model

Run on: June 6, 2006, 21:58:15 ; Search time 41 Seconds
(without alignments)
1044.304 Million cell updates/sec

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Maximum Match 100%
Listing first 45 summaries

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3: pir3.*
4: pir4.*

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SUMMARIES

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4	177.5	7.7	574	2 T41068	hypothetical prote
5	163	7.0	539	2 S67049	probable membrane
6	126	5.4	372	2 S52054	ubiquinol-cytochro
7	119	5.1	523	2 T11916	NADH2 dehydrogenas
8	118.5	5.1	619	2 T11314	NADH2 dehydrogenas
9	118	5.1	497	1 S53834	NADH2 dehydrogenas
10	117.5	5.1	338	2 S50339	NADH2 dehydrogenas
11	115	5.0	868	2 E89897	conserved hypothet
12	113	4.9	633	2 G95385	Kup2 potassium upt
13	111	4.8	493	2 S78183	NADH2 dehydrogenas
14	110.5	4.8	694	2 E69143	hypothetical prote
15	110	4.8	495	1 S25942	NADH2 dehydrogenas
16	109	4.7	501	2 B71707	ADP-ATP carrier pr
17	108.5	4.7	608	2 C70111	V-type ATPase, sub
18	108	4.7	474	2 B64232	hypothetical prote
19	108	4.7	1783	2 T37258	probable voltage-d
20	108	4.7	1917	2 AG8728	protein C48A7.1 [i
21	107.5	4.6	447	2 AG0377	probable O-unit fl
22	107.5	4.6	627	2 D90452	hypothetical prote
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26	106	4.6	495	2 T12401	NADH2 dehydrogenas
27	106	4.6	497	1 WMBELM	membrane protein L
28	106	4.6	503	2 D70930	hypothetical prote
29	106	4.6	677	2 T50022	sulfate transporte

30	105.5	4.6	332	2 B82876	oligopeptide trans
31	105	4.5	782	2 T25925	hypothetical prote
32	104.5	4.5	342	2 T29245	hypothetical prote
33	104.5	4.5	475	2 S73746	MG294 homolog A05
34	104.5	4.5	492	2 E58931	NADH2 dehydrogenas
35	104	4.5	245	2 B60944	ubiquinol-cytochro
36	104	4.5	445	2 E22845	hypothetical prote
37	104	4.5	544	2 C96943	uncharacterized me
38	103.5	4.5	250	2 C60944	ubiquinol-cytochro
39	103	4.4	446	2 S01187	NADH2 dehydrogenas
40	103	4.4	461	2 S60253	sel-12 protein - C
41	103	4.4	518	2 A53207	probable folate tr
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ALIGNMENTS

RESULT 1

T16254
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C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T16254
R;Wu, X.
submitted to the EMBL Data Library, November 1995
A;Description: The sequence of C. elegans cosmid F35C8.
A;Reference number: Z18486
A;Accession: T16254
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-771 <WUX>
A;Cross-references: UNIPROT:Q20026; UNIPARC:UPI000007C755; EMBL:U40941; NID:gi072184; PIR
C;Genetics:
A;Gene: CESP:F35C8.7
A;Introns: 87/2; 143/2; 238/1; 289/2; 428/2; 629/3; 678/1; 712/1; 736/1

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Qy	218	SUSILFFYHQGTGVKSGFLISVVRIPRIIVMYNQNALKEQHGALSRYLPRCCYCCFWCL	277				
Db	557	ALNRAIRYNLGSAFAGSLIIAIVKIIRVLEIYDHKLKGSQNKAKWFLM-CLKKCCFWCL	615				
Qy	278	DKVLLHNLQNYTTTAINGTDFCTSAKAPKILSKNSSHFTSINCFGDFIIFGLKVLVC	337				
Db	616	EYFFKFLTKNAYIMIAIYGNPFSSAKDSFLLRITNIRVTVVVKVAGILLFLFKGSMI--	673				
Qy	338	FTVFGGLMAFNYNRAQV-----WAVPLLVAFAYLVAHSLFSLSVFETVLDAIF	386				
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RESULT 2
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C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
A;Accession: T05692
R;Revan, M.; Wedler, H.; Kutzner, M.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Mayer, K.F. submitted to the Protein Sequence Database, February 1999
A;Reference number: Z15420
A;Accession: T05692
A;Molecule type: DNA
A;Residues: 1-523 <BEV>
A;Cross-references: UNIPROT:Q9S2P2; UNIPARC:UPI000000A31F2; EMBL:AL035540
A;Experimental source: Cultivar Columbia; BAC clone F20M13
C;Genetics:
A;Map position: 4
A;Introns: 264/2; 339/2; 391/1; 437/3
A;Note: F20M13.200

Query Match 11.1%; Score 257.5; DB 2; Length 523;
Best Local Similarity 24.6%; Pred. No. 1.2e-13;
Matches 100; Conservative 75; Mismatches 160; Indels 71; Gaps 16;

QY 6 TILGCLIALALSLAMWTFRTITLLVHIFISLVILGLLFVCGVLMWLYDYNDLSIE 65
Db 145 TLVVTILSVPPFCFVLLLLKHVTQIVACPLFLVLPPIFF-NVYVFACTLSLSSCSDA 203

QY 66 LQTERENMKVGLGFAIVSTGITAIVLLVFLVKRIKLTVELFQITNKALISSAPFLLPQ 125
Db 204 LPLAYRILVLFVFLII-----GIIVHIIIVANWHRIDLTQIISVASDALS-----KN 251

QY 126 LMTFAILIFPWLVAVLSLGTAGAAQVME-GGQ--VEYKPLSGIRYMWSYHLIGLIWT 182
Db 252 LKLFVVL-----PLLTGFGKVFVPELDQGFCEWKEDSWPYYALAILTWS 302

QY 183 SEFILACQOMTIAGAVVTCYFNRSKNDP--PDHPILSSLSILFFYHQGTVVGKSFSLISVVR 241
Db 303 LAVVEMQVYVVISGAIQAQYF--SKEDSIKKIRSLRNFAQSGSFGTICVSGLLICIVR 360

QY 242 IPRILVYMQNALKEOHGALSRYLPRCCYCCFWCLDKYLLHLNQNAYTTTAINGTDFCT 301
Db 361 VVRAIV--DNAREENTQGIIVNVL-RCC-----ANALLGEAYCT 396

QY 302 SAKDAFKILSKN--SSHF-----TSINCFGDFIIFLGKVLVWCFTVFGGLMAF--NYNR 351
Db 397 SAKWTYELLRLNLLSAVFVETVSTRI-LTGIVFVLSAAYAVATWAVLRGVSNLGDYSYV 455

QY 352 AFQWAVPLLLVAFFAYLVAHVSFLSFVETVLDALFICFAVDLETND 397
Db 456 AVLAWVLLIVILAFVH-----VLDDVIDTIYVCYAIKDRDKGD 493

RESULT 3
C86385
hypothetical protein F2J7.7 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: C86385
R;Theologas, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.K.; Creasy, T.H.; Dewar, K.;ansen, N.F.; Hughes, B.; Huizlar, L. Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Luros, J.S.; Maiti, R.; Marziali,ker, M.; Salzborg, S.B.; Schwarz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712

A;Accession: C86385
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-488 <STO>
A;Cross-references: UNIPROT:Q9C6L9; UNIPARC:UPI000000A87B5; GB:AE005172; NID:gl0092332; P;J
C;Genetics:
A;Map position: 1

Query Match 7.7%; Score 179; DB 2; Length 488;
Best Local Similarity 21.1%; Pred. No. 3.6e-07;
Matches 85; Conservative 62; Mismatches 146; Indels 110; Gaps 18;

QY 21 MMFTFRITLLVHIFISLVILGLLFVCGVLMWLYDYNDLSIELDTERENMKCVLGFA 80
Db 128 MKVSVHILTYLA-----VSVLCFCWCLFFW-----GGA 157

QY 81 IVSTGITAVLLVL-----IFVLRKRIKLTVELFQITNKALISSAPFLLPQPLWTFAL 131
Db 158 FAVGSLLOFLYVISVIDRLPFTMLVRKALKLVWGLPKVIMVA-----HAFTV 205

QY 132 LIFFVW-LWAVALLSLGTAGAAQVMEGGQVEYKPLSGIRYMWSYHLIGLIWTSEFTLACQ 190
Db 206 VMLLMWSLW-----SFGAAGVASSMGDE-----GRWLLVVLVSFLWTCGAVLCNTV 253

QY 191 QMTIAGAVVTCYFNRSKNDP--PDHPILSSLSILFFYHQGTVVGKSFSLISVVRIPRIIV 247
Db 254 HVIVSGWVHVLPHCQVESSSIPSSSLVDSLRYAVTTSGSICYGSLFTAAIR----- 307

QY 248 MYMQNALKEOHGALSRYLPRCCYCCFWCLDKYLLHL-----NQNAYTTTAINGTDF 299
Db 308 -----TLRWEIRGFRSKICGNECLLC--CVD-FLFHLVETLVRFFNKYAVQIAYVYKGF 359

QY 300 CTSAKDAFKIL-SKNSHETSINCFGDFIIFLGKVLVWCFTVFGGLMAFNRYNRAFOVWA- 357
Db 360 NKSARDAWELFQSTGVLEALVAYDCSG-AVLLMG-----TIFGGTIT---GSCIGINAW 408

QY 358 -----VPLLVAFAFAYLVAHVSFLS-----VFETVLDALFLCFAVD 392
Db 409 IKYSDRIVINVASTAMLGMVGLVGLGMVVESAVTSIYICFAED 451

RESULT 4
T41068
hypothetical protein SPCC1682.11c - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T41068
R;Murphy, L.; Harris, D.; Lyne, M.; Rajandream, M.A.; Barrell, B.G. submitted to the EMBL Data Library, September 1998
A;Reference number: Z21968
A;Accession: T41068
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-574 <MUR>
A;Cross-references: UNIPROT:O74441; UNIPARC:UPI000006ABD2; EMBL:AL031525; PIDN:CAA20677.1
A;Experimental source: strain 972h; cosmid c1682
C;Genetics:
A;Gene: SPDB.SPCC1682.11c
A;Map position: 3
A;Introns: 5/1; 358/2; 538/2
C;Superfamily: Schizosaccharomyces pombe hypothetical protein SPCC1682.11c

Query Match 7.7%; Score 177.5; DB 2; Length 574;
Best Local Similarity 21.4%; Pred. No. 5.7e-07;
Matches 91; Conservative 76; Mismatches 159; Indels 99; Gaps 20;

QY 12 ILALALSAMWTFRTITLLVHIFISLVILGLLFVCGVLMWLYDYNDLSIELDTERE 71
Db 192 IICMMLSVIIVLFCVLAIPRFLYELLASVPLTMFAFAVYLL-----KASRIHLETSIQ 243

QY 72 NMKCVLGFAIVSTGI---TAVLLVILFVLKRI--KLTVELFQITNKALISSAP-----EL 121
Db 244 PKLMELI-----TGIILLVAPILLSYVWRRRIHFETSFNIRLACKRVADIPOITLIFI 297

Db 248 ----CIYW-----FFVHEESWIIIVDTLTKSDKILPEWFFLSFFGFLKSPDKF----- 292

QY 315 SHETSINCFGDFIIFLGKVLVVCFTVE-----GGMAFNYNRAFOVWAVPLLLVAFAYLV 370

Db 293 -----MGLFLFLF-----VLCFAUFLFILNCILFIYCRSLLW-MSLSLVLFY-YLC 337

QY 371 AHSFSLSVFETVLDALFLCAVDLE 394

Db 338 VGGFLSLY-----VVLCPFLLWME 355

RESULT 7

Tl1916

NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 - Prototheca wickerhamii mitochondrion

C;Species: mitochondrion Prototheca wickerhamii

C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004

C;Accession: Tl1916

R;Wolff, G.; Plante, I.; Lang, B.F.; Kueck, U.; Burger, G.

J. Mol. Biol. 237, 75-86, 1994

A;Title: Complete sequence of the mitochondrial DNA of the chlorophyte alga Prototheca wickerhamii

A;Reference number: Z17373; MUID:94180393; PMID:8133522

A;Accession: Tl1916

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-523 <WOL>

A;Cross-references: UNIPROT:Q37617; UNIPARC:UPI0000130787; EMBL:U02970; NID:g467843; PID:11916

A;Experimental source: strain HB-8

C;Genetics:

A;Genome: mitochondrion

A;Note: nad4

C;Superfamily: NADH dehydrogenase (ubiquinone) chain 4

C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match 5.1%; Score 119; DB 2; Length 523;

Best Local Similarity 18.1%; Pred. No. 0.037;

Matches 76; Conservative 63; Mismatches 163; Indels 118; Gaps 15;

QY 11 CILALALSAMMTFRFITLLVHIFISVLILGILGVLWGLWLYDYDNDLSIELDTER 70

Db 151 CIAFLVLETUMLTVFSLVDLLLFYIFESVLIPFIIIGV-WG-----SRER 196

QY 71 ENMKCVLGAIVGTAVLLVFLVRKRIKLTVELFQITNKAISSAPFLFQPLWTFA 130

Db 197 KIRAAQFFLYTLFGSLVLMALAILLYFQGTLDIEMLYLSDFSERQCILWLAFASFA 256

QY 131 IL-----IPFW-----VLWAVLLSLGTAG-----AAQWEGGQVYKPLSGI 168

Db 257 VKVMPVPVHIWLPFAHVEAPTAGSVILAGILLKLTGYGLRFSIPLFPYACIYFTPL--- 313

QY 169 RYMWSYHLGLIWTG-----EFILACQMTIAGAVVTCYFNRSKNDPPDHPILSSL 219

Db 314 --IYTWSVIAIVTSCTRIQLDKLIIAYSSVAHNMNFVTIGLSQNT----- 359

QY 220 SILFFYHQGVWKGSLISVVVRIPRIIVMYMQNALKEQHGALSRYLFRCCYCCFWCLDK 279

Db 360 -----QG---IGSILLMI-----SHGLVSPALFLCVGLVY----- 387

QY 280 YLLHLNQNAVTTAINGTDFTCSAKDAFKILSKNSHFTSINCF-----GDFIIFLG 331

Db 388 -----DRHKTRLLRYSGCGTQMPIFALL---FVFFTMANISLPGTSFPGFEFLVFIG 437

QY 332 KVLVVCFTVFGGLMAFNYNRAFOVWAVPLLLVAFAYLVNAH-SFLSVFETVLDALFLCPA 390

Db 438 SYQNNSFVAFCAATGMVLGAAYALNLCNRLI-----YGVSKPDFINTWSDVNRREFMFA 492

RESULT 8

Tl1314

NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Pedinomonas minor mitochondrion

C;Species: mitochondrion Pedinomonas minor

C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004

C;Accession: Tl1314

R;Turmel, M.; Lemieux, C.; Burger, G.; Lang, B.F.; Otis, C.; Plante, I.; Gray, M.W.

submitted to the EMBL Data Library, December 1998

A;Description: The complete mitochondrial DNA sequences of Nephroselmis olivacea and Pedicellina olivacea

A;Reference number: Z17261

A;Accession: Tl1314

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-619 <TUR>

A;Cross-references: UNIPROT:Q9ZY28; UNIPARC:UPI000008C2A6; EMBL:AF116775; NID:g4378766; I

C;Genetics:

A;Genome: mitochondrion

A;Genetic code: SGC3

A;Note: nad5

C;Superfamily: NADH dehydrogenase (ubiquinone) chain 5

C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match 5.1%; Score 118.5; DB 2; Length 619;

Best Local Similarity 22.0%; Pred. No. 0.048;

Matches 105; Conservative 73; Mismatches 160; Indels 139; Gaps 24;

QY 7 ILGLCILALALSAMMTFRFITL-LLVHIFIS-----LVLIG 43

Db 124 ILVLVSENALTFLGWEIGITSYLLINFWISKLOSGLSAKAVFLNRIGSFFIALG 183

QY 44 LLFVCGVLWMLYDYDNDL-----SIELDTERENMK-CVLGFAIVSTGITAVLLVLFVLR 98

Db 184 LTF-----YLFSGDDLFLISSLSVFEKQIVKYLIIAYLIASTAKSAQILLHW-LP 234

QY 99 KRIKLTVELFQITNKA--ISSAPFLFQPLWTFAILFF-----WVLWAVLISL--GTAG 150

Db 235 DAIEAPTVPVSSLLHAATLVGAGVYLIIK--LSFLSLDDSSNFIIVIGILTSFLAGLIG 292

QY 151 AAQWEGGQVYKPLSGIRYMSYHLGLI-----WTSEFILLACQMQTIAGAVVTCY 202

Db 293 FNOFTDKRIIAVSTCSQIGLM--FYAIGLISLDFSVLHVFVKLMFLAGAFIHI 350

QY 203 FNRSKNDPPDHP-----ILSLSIL-PFYHQGTVVKGSFSLISVVVRIPRIIVM 248

Db 351 FN--EQDIRKYGLNLFNLSFLAFVLSNLSLGIFFIAGFYSKELLISGI----- 400

QY 249 YMQNALKEQHGALSRYLFRCCYCCFWCLDKVLLHLNQNAVTTAINGTDFTCSAKDAFK 308

Db 401 YNN-----FWSL-----LSVLAIFTTCIYG-----IKSILL 427

QY 309 IL--SKNSHFTSINCFGD--FTIFLGKVLVVCFTVFG-----GLMAFNYNRAFOVWA 357

Db 428 VLSGSPNWSFFSITTYDNLVIIILSVLNLNFFFGPMITEQIKLMDIVYNS----- 482

QY 358 VPILLVAFAYLVNAHSFSLSVFETVLDALFLCAVDLETNDSSEKPYFMDQBFSLFV 414

Db 483 -----VFVS---IKSNLFLFEHVYVNWILLFVISVFLILSNWYSIFFFSKSLSFI 530

RESULT 9

S53834

NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 - Acanthamoeba castellanii mitochondrion

C;Species: mitochondrion Acanthamoeba castellanii

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C;Accession: S53834

R;Burger, G.; Plante, I.; Loneragan, K.M.; Gray, M.W.

J. Mol. Biol. 245, 522-537, 1995

A;Title: The mitochondrial DNA of the amoeboid protozoan, Acanthamoeba castellanii: complete sequence

A;Reference number: S53825; MUID:95147275; PMID:7844823

A;Accession: S53834

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-497 <BUR>

A;Cross-references: UNIPROT:Q37375; UNIPARC:UPI000013072D; GB:U12386; NID:g562028; PIDN:7

A;Experimental source: strain Neff; ATCC 30010

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1994

C;Genetics:

A;Genome: mitochondrion

A;Genetic code: SGC6

C;Superfamily: NADH dehydrogenase (ubiquinone) chain 4

DD
42 -----1PVMVQKSTSEEB5GVAIFLV--QAVOSARLFFFGGEMTNNMTTCCWELNLT 83

Db 504 NSPFIYHNGISLYSIFNGDILKYDKTLQI 535

RESULT 12

G95385

Kup2 Potassium uptake protein [imported] - Sinorhizobium meliloti (strain 1021) magaplas

C;Species: Sinorhizobium meliloti

C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004

C;Accession: G95385

R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows

; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.

Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001

A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti

A;Reference number: A95262; MUID:21396509; PMID:11481432

A;Accession: G95385

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-633 <KUR>

A;Cross-references: UNIPROT:Q92Y93; UNIPARC:UPI00000D4778; GB:AE006469; PIDN:AAK65649.1;

A;Experimental source: Strain 1021, megaplasmid pSymba

R;Galibert, F.; Finan, T.M.; Long, S.R.; Fuller, A.; Abola, P.; Ampe, F.; Barloy-Hubler,

peia, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;

L.; Hyman, R.W.; Jones, T.

Science 293, 668-672, 2001

A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, B.; Komp, C.; Lelaure,

hebaull, P.; Vandenbol, M.; Vorholter, E.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.

A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.

A;Reference number: A96039; MUID:21368234; PMID:11474104

A;Contents: annotation

C;Genetics:

A;Gene: kup2

A;Genome: plasmid

Query Match 4.9%; Score 113; DB 2; Length 633;

Best Local Similarity 22.0%; Pred. No. 0.14;

Matches 49; Conservative 39; Mismatches 67; Indels 68; Gaps 9;

QY 3 GRDTILGLCTIALALSAMMFFRFTTL-----VHFFISLVILG-----LLFV 47

Db 54 GRDEIGLVSLV-WTLTAIVTIKYFLLRANDGEGGTLGLALLKKGTQKPYLMFF 112

QY 48 CGVLWMLY-----DYTNDSIELDTERENMKCVLGFIVSTG-----ITAVLLVLIFV 96

Db 113 AGVLGAALFGDAMIPLSV-----LSAVEGLKLVAPLHDYVLPISVVIILLFA 164

QY 97 LRKRIKLTVELFOITNKAISSAPFLFQPLWTFAILIFFWLVWVALLSLGTAGAAQWME 156

Db 165 VQSR-----GTGAVSVFFGPITLVWFLWMAAGVAHIGD 198

QY 157 GGQV--EYKPLSGIRYMWVHLGLIWTSEFILACQOMTIAGA 197

Db 199 DLALSAFNPLNAGFLWNLGLIGFI-----VLGAIFLVTIGA 236

RESULT 13

S78183

NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 - Reclinomonas americana (ATCC 503

C;Species: mitochondrion Reclinomonas americana

A;Variety: ATCC 50394

C;Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 09-Jul-2004

C;Accession: S78183

R;Lang, B.F.; Burger, G.; O'Kelly, C.J.; Cedergren, R.; Golding, G.B.; Lemieux, C.; Sank

Nature 387, 493-497, 1997

A;Title: An ancestral mitochondrial DNA resembling a eubacterial genome in miniature.

A;Reference number: S78127; MUID:97311393; PMID:9168110

A;Accession: S78183

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-493 <LAN>

A;Cross-references: UNIPROT:O21286; UNIPARC:UPI000008D0BD; EMBL:AF007261; NID:G2258325;

A;Experimental source: ATCC 50394

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1997

C;Genetics:

A;Gene: nad4

A;Genome: mitochondrion

A;Superfamily: NADH dehydrogenase (ubiquinone) chain 4

C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match 4.8%; Score 111; DB 2; Length 493;

Best Local Similarity 21.8%; Pred. No. 0.16;

Matches 85; Conservative 53; Mismatches 128; Indels 124; Gaps 21;

QY 10 LCILALALSAMMFFRFTTLVHIFISLVILGGLFVCGVLWMLYYDYTNDSIELDTE 69

Db 120 ICFLLDALLIMTFC--VLDLVLFIFFESVLIPMFIQV-WG-----SRE 163

QY 70 RENMKCVLGFIVSTGITAVLVLVFL-----RKRIKLTVELFOITNKAISSAPFL 122

Db 164 KRVRAAYMLFLTYTFG-SULMLIAIMVIYFDAGTTDQIVLLTFESQERQKLWLAF 222

QY 123 FQ---PLMTFAILIFFW-----VLWVAVLLSLGTAG-----AAQVMEGQVVE 162

Db 223 FAIKIPMVFPVH---WLPEAHVEAPTAGSVLLAGVLLKGGVILRFSIPMPEATVVF 278

QY 163 KPLSGIRYMWVHLGLIWTSEFILACQOMTIAGAVVTCYFNRSKNDDPDHPILSL 222

Db 279 TPL-----VYTMSSIIAIYTS--LTLRQIDLKRIIA-----YSSVA-- 313

QY 223 FFVHQGTVVKGSFLISVVRIPRIIVYMQNALKEQHQHGSRLVLRCCYCCFWCLDKY-- 280

Db 314 ---HMFVTIGFSLNMQGLEGSILLML-----SHGIVSSALFICIGVLY--DRHKT 360

QY 281 -LHLNQNAYTTTAINGTDFC--TSAKDAFKILSKNSHFTSINCFDGFIIIFLGKLVVVC 337

Db 361 RLLKYYSGVVQIMPFIATLFLMLFTWA---NISLPGTSSEFV-----GEFLVLIG----- 405

QY 338 FTVFGGLMAFNVRAPQWVAVPVLVAFPA 367

Db 406 -----AFNSNTT-----VAFPA 417

RESULT 14

E69143

hypothetical protein MTH339 - Methanobacterium thermoautotrophicum (strain Delta H)

C;Species: Methanobacterium thermoautotrophicum

C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004

C;Accession: E69143

R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;

; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.;

ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.

J. Bacteriol. 179, 7135-7155, 1997

A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: functi

A;Reference number: A69000; MUID:98037514; PMID:9371463

A;Accession: E69143

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-694 <MTH>

A;Cross-references: UNIPROT:O26439; UNIPARC:UPI0000062C5F; GB:AE000818; GB:AE000666; NID:

A;Experimental source: strain Delta H

C;Genetics:

A;Gene: MTH339

Query Match 4.8%; Score 110.5; DB 2; Length 694;

Best Local Similarity 20.5%; Pred. No. 0.25;

Matches 88; Conservative 73; Mismatches 164; Indels 105; Gaps 20;

QY 12 ILALALSAMMFFRFTTLVHIFISLV-----LGLLFVCGVLWMLY----- 56

Db 58 VIAAALSIFLM---MMTGLIINSFPLMRPLSLPILSAINLLII--ALMVYHLRGE 111

QY 57 ----DYTNDSIELDTERENMKCVLGFIVS--TGITAVLVLVIFVLRKRIKLTVELFQ 109

Db 112 EPLNLKASGNLSTALSSILFPVLTVIGSVLMKNYSVNTVLLVLLF-----IPVYILLE 166

QY 110 ITNKAISSAPFLFQPLWTFAILIFFWLVWVAVLSLGTAGAAQWMEGQVVEKPLSGIR 169

```
Db 167 VFKKKGIPA-----TYPVAIF-----SISLSL-----LIMNGLPSNY--LIGRD 203
QY 170 YMSYHYLIGL-----IWTSEFILACQOMTIAGAVVTCYFNRSKNDDPPDHPILSSL 219
Db 204 IHMEFYLFKALMAHHMDHMGVSYNAYNACLSTVTLFVVIYKVLN-----VPEV 252
QY 220 SILFFYHQGTGVKGSFLISVVRIPRIIWMYQNALKEQHGALSRYL-----FRCCYCCFW 275
Db 253 YIFKFFY-----GFIGALMPLP--VYLISERILKRSYGFYATLLFIQFSFIYILGW 303
QY 276 CLDKYLLHLNQNAVTTTAINGTDFCTSAKDAFKILSKNS--SHFTSINCFGDFTIFLQKV 333
Db 304 C--ROLVALLFFAAAVMLTGMRRSHKLLFVFMVGTVLVSHVTTAYVF-----FFLVAL 357
QY 334 LVVCFTVFGGLMAFNYNRAF--QVMVAPLLLVAFAYLVA-----HSFLSVFETVLDAIF 386
Db 358 IPILVRVMKRLKVPDDSKGFFAASLAVLFFVVFVFAWYAQTGAPFKSAVSFTTKTLRMS 417
QY 387 LCFADVLETN 396
Db 418 EFFSADMRN 427

RESULT 15
S25942
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 - liverwort (Marchantia polymorpha)
N;Alternate names: NADH-ubiquinone oxidoreductase chain 4
C;Species: mitochondrion Marchantia polymorpha
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S25942; S31172
R;Oda, K.; Yamato, K.; Ohta, E.; Nakamura, Y.; Takemura, M.; Nozato, N.; Akashi, K.; Kan
J. Mol. Biol. 223, 1-7, 1992
A;Title: Gene organization deduced from the complete sequence of liverwort Marchantia po
A;Reference number: S25941; MUID:92114051; PMID:1731062
A;Accession: S25942
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-495 <ODA>
A;Cross-references: UNIPROT:P26848; UNIPARC:UPI0000130771; EMBL:M68929; NID:G786182; PID
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1992
R;Nozato, N.; Oda, K.; Yamato, K.; Ohta, E.; Takemura, M.; Akashi, K.; Fukuzawa, H.; Ony
Mol. Gen. Genet. 237, 343-350, 1993
A;Title: Cotranscriptional expression of mitochondrial genes for subunits of NADH dehyd
A;Reference number: S31171; MUID:93247547; PMID:8483448
A;Accession: S31172
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-495 <NOZ>
A;Cross-references: UNIPARC:UPI0000130771; EMBL:M68929; NID:G786182; PIDN:AAC09398.1; PI
C;Genetics:
A;Gene: nad4
A;Genome: mitochondrion
A;Introns: 183/2
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 4
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match 4.8%; Score 110; DB 1; Length 495;
Best Local Similarity 18.9%; Pred. No. 0.19;
Matches 78; Conservative 73; Mismatches 152; Indels 110; Gaps 16;

QY 12 ILALALSAMMFTFRFTITLLVHIFISLVILG-----LLFVCGVL 51
Db 130 LIAVFCSLDLLIFVVFESVLIPMFIIGVMSQRKKAAYQFFLYTLMGSLFMLLAIL 189
QY 52 WLYYDYNDLSIELDERENMKCVLGFVAIVSTGITAVLLVLPVLRKRIKLTVELFQIT 111
Db 190 FIFFQTCTDQLLTTE-----FSERQILLMTIAFFASF 224
QY 112 NKAISSAPFLFQPLWTFAILIFFWLWVAVLLSLGTAG-----AAQWMEGQVEYKPLSG 167
Db 225 SVKVPVPIVHLPDEAHVEAPTAGSVILAGILLKLTGYFLRFSIPNPEATLYFTP--- 281
QY 168 IRYMWSYHLIGLIWTSEFILACQOMTIAGAVVTCYFNRSKNDDPPDHPILSSLILFFYHQ 227
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Db 282 --FIYTLSVIAIITYS--LTTIRQIDLKIIA-----YSSVA-----HM 316
QY 228 GTVVKGSFLISVVRIPRIIWMYQNALKEQHGALSRYLFRCCYCCFWCLDKY---LLHL 284
Db 317 NFVTIGMFSLNIQIEGSIILLML-----SHGLVSSALFLCVGALY---DRHKTRIVKY 366
QY 285 NONAYTTTAINGTDFCTSAKDAFKILSKNSHFTSINCFGDFTIFLG-----KVLVVCFTV 340
Db 367 YGGLVSTMPITFTIF-----LFFTLANMSLPCTS-SFIGEFLILVGAFQNSILVATLAA 419
QY 341 FGGIMAFNYNRAFQVMVAPLLLVAFEA--YLVASHFLSVFETVLDLALFLCFVAV 391
Db 420 LGMIL-----GAAYSLMLYNRVFGNFKPNFILKFSDLNRREVLI--IFLFFIV 465
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Search completed: June 6, 2006, 22:03:49
Job time : 43 secs

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Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

Page Blank (uspto)

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 6, 2006, 21:54:45 ; Search time 298 Seconds
(without alignments)
1381.315 Million cell updates/sec

Title: US-10-063-537-32

Perfect score: 2315

Sequence: 1 MSGRDTILGLIALALSLA.....QQDKSLRNEEGTELOAIVR 445

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 7.2.2*
1: uniprot_sprot*
2: uniprot_trembl*
SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	ID	Description
1	2314	99.9	605	2 Q7Z6C5_HUMAN	Q7Z6C5 homo sapien
2	2314	99.9	653	1 CTLL3_HUMAN	Q8n4m1 homo sapien
3	1857	80.2	652	1 CTLL3_MOUSE	Q921v7 mus musculu
4	1854.5	80.1	604	1 CTLL3_RAT	Q6ay52 rattus norv
5	1147.5	49.6	651	2 Q63Z53_XENLA	Q63z53 xenopus lae
6	1146.5	49.5	651	2 Q6IR74_XENLA	Q6ir74 xenopus lae
7	1131	48.9	656	1 CTLL1_RAT	Q8vii6 rattus norv
8	1121	48.4	657	1 CTLL1_HUMAN	Q8wwi5 homo sapien
9	1116	48.2	646	1 CTLL1_TORMA	Q919b9 torpedo mar
10	1113	48.1	653	1 CTLL1_MOUSE	Q6x893 mus musculu
11	696.5	30.1	493	2 Q7PV56_ANOGA	Q7pv56 anopheles g
12	678	29.3	677	2 Q7QR7_ANOGA	Q7q5r7 anopheles g
13	624.5	27.0	691	2 Q86P33_DROME	Q86p33 drosophila
14	624.5	27.0	691	2 Q9VZE7_DROME	Q9vze7 drosophila
15	611	26.4	707	2 Q6GN42_XENLA	Q6gn42 xenopus lae
16	604.5	26.1	710	2 Q6IP59_XENLA	Q6ip59 xenopus lae
17	604.5	26.1	863	2 Q4S752_TETNG	Q4s752 tetraodon n
18	599.5	25.9	704	1 CTLL2_MOUSE	Q8by89 mus musculu
19	594.5	25.7	711	1 CTLL2_PONPY	Q5r519 pongo pygma
20	593.5	25.6	697	2 Q7SYC9_BRARE	Q7sy9c brachydanio
21	593.5	25.6	705	1 CTLL2_CAVPO	Q810f1 cavia porce
22	592.5	25.6	723	2 Q7T3E0_BRARE	Q7t2b0 brachydanio
23	590.5	25.5	706	1 CTLL2_HUMAN	Q8iwa5 homo sapien
24	583.5	25.2	656	2 Q4T6N2_TETNG	Q4t6n2 tetraodon n
25	571	24.7	628	2 Q54148_DICDI	Q54148 dictyosteli
26	568	24.5	675	2 Q4G0K0_HUMAN	Q4g0k0 homo sapien
27	567	24.5	719	1 CTLL5_HUMAN	Q8ncs7 homo sapien
28	555	24.0	717	1 CTLL5_MACFA	Q95jw2 macaca fasc
29	544	23.5	710	1 CTLL5_MOUSE	Q5rj12 mus musculu
30	539	23.3	710	1 CTLL4_HUMAN	Q35gd3 homo sapien
31	538.5	23.3	555	2 Q3TL93_MOUSE	Q3tl93 mus musculu

32	538.5	23.3	707	1 CTLL4_MOUSE	Q91val mus musculu
33	538.5	23.3	707	1 CTLL4_MOUSE	Q91val mus musculu
34	537.5	23.2	707	1 CTLL4_RAT	Q6mg1 rattus norv
35	521.5	22.5	749	2 Q4RIZ5_TETNG	Q4riz5 tetraodon n
36	513	22.2	796	2 Q9VAP3_DROME	Q9vap3 drosophila
37	509	22.0	773	2 Q618G3_CABER	Q618g3 caenorhabdi
38	505	21.8	730	2 Q8M062_CABER	Q8mq62 caenorhabdi
39	505	21.8	771	2 Q20026_CABEL	Q20026 caenorhabdi
40	497.5	21.5	765	2 Q7PRJ0_ANOGA	Q7prj0 anopheles g
41	439	19.0	311	2 Q6NVE7_MOUSE	Q6nve7 mus musculu
42	428	18.5	288	2 Q6UX89_HUMAN	Q6ux89 homo sapien
43	421	18.2	344	2 Q5CZQ9_BRARE	Q5czq9 brachydanio
44	382	16.5	711	2 Q7X668_ORYSA	Q7x668 oryza sativ
45	377	16.3	711	2 Q7XPX3_ORYSA	Q7xpx3 oryza sativ

ALIGNMENTS

RESULT 1
Q7Z6C5_HUMAN PRELIMINARY; PRT; 605 AA.
AC Q7Z6C5;
DT 01-OCT-2003, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2003, sequence version 1.
DT 07-FEB-2006, entry version 12.
DE Hypothetical protein SLC44A3.
GN Name=SLC44A3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Colon.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Scapleton M., Soares M.B., Donald M.P., Casavant T.L., Scheetz T.E., Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnarch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
RT	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RL	[2]
RP	NUCLEOTIDE SEQUENCE.
RC	TISSUE=Colon;
RG	NIH MCC Project;
RL	Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
CC	Copyrighted by the Uniprot Consortium, see http://www.uniprot.org/terms
CC	Distributed under the Creative Commons Attribution-NoDerivs License
CC	-----
DR	EMBL; BC053877; AH53877.1; -; mRNA.
DR	Ensembl; ENSG00000143036; Homo sapiens.
DR	LinkHub; Q7Z6C5; -
DR	InterPro; IPR007603; DUF580.
DR	PANTHER; PTHR12385; DUF580; 1.
DR	Pfam; PF04515; DUF580; 1.
KW	Hypothetical protein.

SQ SEQUENCE 605 AA; 68047 MW; 1182534F9556DADD CRC64;

Query Match 99.9%; Score 2314; DB 2; Length 605;
 Best Local Similarity 99.8%; Pred. No. 2.8e-166;
 Matches 444; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSGRDITLGLCILAALSLAMMTFFRITTLVHIFISLVILGLLFVCGVGLWLVYDYTN 60
 DB 161 MSGRDITLGLCILAALSLAMMTFFRITTLVHIFISLVILGLLFVCGVGLWLVYDYTN 220

QY 61 DLSIELDTERENMKCVLGFPAIVSTGTAVLLVLIIFVLRKRIKLTVELFOITNKAISSAPP 120
 DB 221 DLSIELDTERENMKCVLGFPAIVSTGTAVLLVLIIFVLRKRIKLTVELFOITNKAISSAPP 280

QY 121 LIFQPLWTFATLIFFFVWLVAVLLSITAGAAQMEGGVVEYKPLSGIRYMSYHLIGLI 180
 DB 281 LIFQPLWTFATLIFFFVWLVAVLLSITAGAAQMEGGVVEYKPLSGIRYMSYHLIGLI 340

QY 181 WTSEFLACQOMTIAGAVTCTVFNRSKNDPPDPHPILSSLSILFFYHOGTVVKGSLISVV 240
 DB 341 WTSEFLACQOMTIAGAVTCTVFNRSKNDPPDPHPILSSLSILFFYHOGTVVKGSLISVV 400

QY 241 RIPRIIVMYQNALKEQHGALSRYLFRCCYCCFWCLDKYLLHLNQNAVTTTAINGTDFC 300
 DB 401 RIPRIIVMYQNALKEQHGALSRYLFRCCYCCFWCLDKYLLHLNQNAVTTTAINGTDFC 460

QY 301 TSAKDAPKILSKNSHFTSINCEGDEIIFLGKVLVVCFTVFGGLMAFNYNRAFOQWAVPL 360
 DB 461 TSAKDAPKILSKNSHFTSINCEGDEIIFLGKVLVVCFTVFGGLMAFNYNRAFOQWAVPL 520

QY 361 LLVAFAYLVAHSFLSVFETVLDALFLCAVDLETNDGSGSEKPYFMDQBFSLSPVKRSNKL 420
 DB 521 LLVAFAYLVAHSFLSVFETVLDALFLCAVDLETNDGSGSEKPYFMDQBFSLSPVKRSNKL 580

QY 421 NNARAQDKHSLRNEGTLEQAIVR 445
 DB 581 NNARAQDKHSLRNEGTLEQAIVR 605

RESULT 2

CTL3_HUMAN STANDARD; PRT; 653 AA.

AC Q8N4W1; Q9BWY7;
 DT 30-AUG-2005, integrated into UniProtKB/Swiss-Prot.
 DT 30-AUG-2005, sequence version 3.
 DE Choline transporter-like protein 3 (Solute carrier family 4 member 3).

GN Name=SLC4A3; Synonyms=CTL3; ORFNames=UNQ558/PRO1115;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RG Human chromosome 1 international sequencing consortium;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC TISSUE=Brain, and Colon;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
 RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Smalilus D.E.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 147-653, AND VARIANT
 RP VAL-438.
 RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
 RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,
 RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
 RA Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
 RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
 RA Lewis L., Liao M.R., Robbie E., Sanchez C., Schoenfeld J.,
 RA Seshagiri S., Simons L., Singh J., Smith V., Stinson J., Vagts A.,
 RA Vandlen R.L., Watanabe C., Wieand D., Woods K., Xie M.-H.,
 RA Vansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
 RA Wood W.I., Godowski P.J., Gray A.M.;
 RT "The secreted protein discovery initiative (SPDI), a large-scale
 effort to identify novel human secreted and transmembrane proteins: a
 RT bioinformatics assessment.";
 RL Genome Res. 13:2265-2270(2003).
 RN [4]
 RP IDENTIFICATION, AND NOMENCLATURE.
 RX MEDLINE=20144127; PubMed=10677542; DOI=10.1073/pnas.030339697;
 RA O'Regan S., Traifford E., Ruat M., Cha N., Compaore D., Meunier F.-M.;
 RT "An electric lobe suppressor for a yeast choline transporter mutation
 belongs to a new family of transporter-like proteins.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:1835-1840(2000).
 CC -!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein (By
 similarity).
 CC -!- SIMILARITY: Belongs to the CTL (choline transporter-like) family.
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL; AC093429; -; NOT ANNOTATED_CDS; Genomic_DNA.
 DR EMBL; ALJ59554; CAC36091.1; -; Genomic DNA.
 DR EMBL; BC033858; AAH3858.2; ALT INIT; mRNA.
 DR EMBL; AY58659; AAQ89022.1; ALT INIT; mRNA.
 DR Ensembl; ENSG00000143036; Homo sapiens.
 DR HGNC; HGNC:28689; SLC4A3.
 DR InterPro; IPR007603; DUF580.
 DR Pfam; PF04515; DUF580; 1.
 DR Membrane; Polymorphism; Transmembrane.
 KW CHAIN 1 653 Choline transporter-like protein 3.
 FT FTId=PRO_0000191720.
 FT TRANSMEM 34 54 Potential.
 FT TRANSMEM 213 233 Potential.
 FT TRANSMEM 243 263 Potential.
 FT TRANSMEM 284 304 Potential.
 FT TRANSMEM 334 354 Potential.
 FT TRANSMEM 384 404 Potential.
 FT TRANSMEM 428 448 Potential.
 FT TRANSMEM 534 554 Potential.
 FT TRANSMEM 563 583 Potential.
 FT VARIANT 438 438 I -> V (in dbSNP:859098).
 FT /FTId=VAR_023405.
 FT CONFLICT 465 465 Missing (in Ref. 1; CAC36091).
 FT SEQUENCE 653 AA; 73797 MW; 54807C920086427B CRC64;

Query Match 99.9%; Score 2314; DB 1; Length 653;
 Best Local Similarity 99.8%; Pred. No. 2.8e-166;
 Matches 444; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSGRDITLGLCILAALSLAMMTFFRITTLVHIFISLVILGLLFVCGVGLWLVYDYTN 60
 DB 209 MSGRDITLGLCILAALSLAMMTFFRITTLVHIFISLVILGLLFVCGVGLWLVYDYTN 268

QY 61 DLSIELTERENMKCVLGFATVSTGITAVLLVLFVLRKRIKLTVELFOITNKAISSAPP 120
 Db 269 DLSIELTERENMKCVLGFATVSTGITAVLLVLFVLRKRIKLTVELFOITNKAISSAPP 328
 QY 121 LLFQPLMTFAILLFFFWLWVAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMWVSYHLIGLI 180
 Db 329 LLFQPLMTFAILLFFFWLWVAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMWVSYHLIGLI 388
 QY 181 WTSEFIIACQOMTITAGAVVTCYFNRSKNDPPDHPILSSLSILFFYHQTIVKGSFLISVV 240
 Db 389 WTSEFIIACQOMTITAGAVVTCYFNRSKNDPPDHPILSSLSILFFYHQTIVKGSFLISVV 448
 QY 241 RIPRIIVMYQNALKEOQHGSALSYLRCVCCVCCFWCLDKYLLHLNQNAYTTAINGTDFC 300
 Db 449 RIPRIIVMYQNALKEOQHGSALSYLRCVCCVCCFWCLDKYLLHLNQNAYTTAINGTDFC 508
 QY 301 TSAKDAFKILSKNSHSTINCFDGFIIIFLGKLVVVCFTVFGGLMAFNRAFOVAVPL 360
 Db 509 TSAKDAFKILSKNSHSTINCFDGFIIIFLGKLVVVCFTVFGGLMAFNRAFOVAVPL 568
 QY 361 LLVAFPAFLVAHSLVSFETVLDALFLCFAVDLETNDGSSEKPYFMDQEFSLFVKRSNKL 420
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 QY 421 NNARAQODKHSRNEEGTELOAIVR 445
 Db 629 NNARAQODKHSRNEEGTELOAIVR 653

RESULT 3

CTLL3_MOUSE
 ID CTLL3_MOUSE STANDARD; PRT; 652 AA.
 AC Q921V7;
 DT 30-AUG-2005, integrated into UniProtKB/Swiss-Prot.
 DT 30-AUG-2005, sequence version 2.
 DT 07-MAR-2006, entry version 27.
 DE Choline transporter-like protein 3 (Solute carrier family 44 member
 DE 3).
 GN Names=Slc44a3; Synonyms=Ctl3;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridea; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC STRAIN=FVB/N; TISSUE=Mammary tumor;
 RX MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -|- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein (By
 CC similarity).
 CC -|- SIMILARITY: Belongs to the CTL (choline transporter-like) family.
 CC

CC 61 DLSIELTERENMKCVLGFATVSTGITAVLLVLFVLRKRIKLTVELFOITNKAISSAPP 120
 CC 269 DLSIELTERENMKCVLGFATVSTGITAVLLVLFVLRKRIKLTVELFOITNKAISSAPP 328
 DR EMBL; BC010552; AAH10552.1; ALT INIT; mRNA.
 DR EMBL; BC025548; AAR25548.1; ALT INIT; mRNA.
 DR Ensemble; ENSMUSG0000039865; Mus musculus.
 DR MGI; MGI:2384860; Slc44a3.
 DR InterPro; IPR007603; DUF580.
 DR Pfam; PF04515; DUF580; 1.
 KW Membrane; Transmembrane.
 FT CHAIN 1 652
 FT TRANSMEM 33 53
 FT TRANSMEM 212 232
 FT TRANSMEM 238 258
 FT TRANSMEM 284 304
 FT TRANSMEM 333 353
 FT TRANSMEM 377 397
 FT TRANSMEM 533 553
 FT TRANSMEM 562 582
 SQ SEQUENCE 652 AA; 73028 MW; A0DA359C7509C8B3 CRC64;

Choline transporter-like protein 3.
 /FtId=PRO_0000191721.

Query Match 80.2%; Score 1857; DB 1; Length 652;
 Best Local Similarity 78.4%; Pred. No. 9.4e-132;
 Matches 349; Conservative 39; Mismatches 57; Indels 0; Gaps 0;

QY 1 MSGRDTILGLCILALSLAMMFTFRITTLVHIFISLVILGLLFCVGVLMWLYDYDTN 60
 Db 208 MAGRDTILGLCVFTFALSAMLFAFRISTLLHIIISLVILGLLFCVGVLMWLYDYDTN 267
 QY 61 DLSIELTERENMKCVLGFATVSTGITAVLLVLFVLRKRIKLTVELFOITNKAISSAPP 120
 Db 268 DLSIELTERENMKCVLGFATVSTGITAVLLVLFVLRKRIKLTVELFOITNKAISSAPP 327
 QY 121 LLFQPLMTFAILLFFFWLWVAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMWVSYHLIGLI 180
 Db 328 LLFQPLMTFAILLFFFWLWVAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMWVSYHLIGLI 387
 QY 181 WTSEFIIACQOMTITAGAVVTCYFNRSKNDPPDHPILSSLSILFFYHQTIVKGSFLISVV 240
 Db 388 WTSEFIIACQOMTITAGAVVTCYFNRSKNDPPDHPILSSLSILFFYHQTIVKGSFLISVV 447
 QY 241 RIPRIIVMYQNALKEOQHGSALSYLRCVCCVCCFWCLDKYLLHLNQNAYTTAINGTDFC 300
 Db 448 RIPRIIVMYQNALKEOQHGSALSYLRCVCCVCCFWCLDKYLLHLNQNAYTTAINGTDFC 507
 QY 301 TSAKDAFKILSKNSHSTINCFDGFIIIFLGKLVVVCFTVFGGLMAFNRAFOVAVPL 360
 Db 508 TSAKDAFKILSKNSHSTINCFDGFIIIFLGKLVVVCFTVFGGLMAFNRAFOVAVPL 567
 QY 361 LLVAFPAFLVAHSLVSFETVLDALFLCFAVDLETNDGSSEKPYFMDQEFSLFVKRSNKL 420
 Db 568 LLVAFPAFLVAHSLVSFETVLDALFLCFAVDLETNDGSSEKPYFMDQEFSLFVKRSNKL 627
 QY 421 NNARAQODKHSRNEEGTELOAIVR 445
 Db 628 NNARAQODKHSRNEEGTELOAIVR 652

RESULT 4

CTLL3_RAT
 ID CTLL3_RAT STANDARD; PRT; 604 AA.
 AC Q6AY92;
 DT 30-AUG-2005, integrated into UniProtKB/Swiss-Prot.
 DT 13-SEP-2004, sequence version 1.
 DT 07-FEB-2006, entry version 16.
 DE Choline transporter-like protein 3 (Solute carrier family 44 member
 DE 3).
 GN Names=Slc44a3; Synonyms=Ctl3;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridea; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;

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RN [1] NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Kidney;
RG NIH - Mammalian Gene Collection (MGC) project;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
RN [2]
RC TISSUE SPECIFICITY.
RC STRAIN=Wistar; TISSUE=Brain;
RX PubMed=15715662; DOI=10.1111/j.1471-4159.2004.02962.x;
RA Traillfort E., Ruat M., O'Regan S., Meunier F.-M.;
RT "Molecular characterization of the family of choline transporter-like
RL J. Neurochem. 92:1116-1125(2005).
CC -|- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein (By
CC similarity).
CC -|- TISSUE SPECIFICITY: Expressed in colon, kidney and ileum.
CC -|- SIMILARITY: Belongs to the CTL (choline transporter-like) family.
CC -----
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CC -----
DR EMBL; BC079142; AAH79142.1; -; mRNA.
DR RGD; 1305808; Ctl3.
DR InterPro; IPR007603; DUF580.
DR PANTHER; PTHR12385; DUF580; 1.
DR Pfam; PF04515; DUF580; 1.
DR Membrane; Transmembrane.
FT CHAIN 1 604 Choline transporter-like protein 3.
FT -----
FT TRANSMEM 165 185 /FTID=PRO_0000191722.
FT TRANSMEM 195 215 Potential.
FT TRANSMEM 237 257 Potential.
FT TRANSMEM 286 306 Potential.
FT TRANSMEM 330 350 Potential.
FT TRANSMEM 485 505 Potential.
FT TRANSMEM 514 534 Potential.
FT TRANSMEM 604 AA; 67679 MW; BA47C3A411CE3E1B CRC64;
SQ SEQUENCE 604 AA; 67679 MW; BA47C3A411CE3E1B CRC64;

Query Match 80.1%; Score 1854.5; DB 1; Length 604;
Best Local Similarity 78.4%; Pred. No. 1.3e-131;
Matches 349; Conservative 37; Mismatches 58; Indels 1; Gaps 1;

QY 1 MSGRDTILGICILALALSAMMFTFTITLLVHIFISVLGLFVCGVLMWLYDYTN 60
DB 161 MAGRDILGICAFVFLSLAMLTFTFTISLTHVHIIISVLGLFVCGVLMWLYDYTN 220
QY 61 DLSIELDTERENKCVLGFVAVSTGTVAVLLVIFVLRKRIKLTVELFQITNKAISSAPF 120
DB 221 DLSIELDTERENKCMKLAFAVITVTVVLLALIFTLRKRVKLTVELLRVTNKAISSRCPF 280
QY 121 LLFQPLWTFAILIFFWVWVAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYVWMSYHLIGLI 180
DB 281 LLFQPLWTFAILIFFWVWVAVLLSLGTAGTAQVMEGGQVEYKPLSGIRYVWYHLIGLI 340
QY 181 WTSEFILACOMTITAGAVVTCYFNRSKNDDPPHPILSSLSILFFYHQTGVVKGSLISVV 240
DB 341 WTSEFILTCQMTVAGWVTCYFNQNDDPPARPILSSLSLTLCYHQTAVKGSLLTWT 400
QY 241 RPIRIIVMYMONALKEQHQGALGRYLFRCYCCYFCWCLDKYLLHLNQNAVYTTAINGTDFC 300
DB 401 RPIRVIFMYIYSTVKE-RHSAPRGEPRCSYCYGLWCLTNPYHLNQDAVAATAINGTDFC 459
QY 301 TSAKDAFKILSKNSHFTSINCEGDTIIFLGKLVVCFYVFGGMAFNYNRAQVAVPL 360
DB 460 TSAKDAHTIISKNSHLSITVNCFGNFIIFLGKLVVCFYVFGGMAFNYNRAQVAVPL 519
QY 361 LLVAFAYLVAHFSVFEVFLDALFLCFVAVDLTNDGSEKPYFMDQFSLFVKRSNKL 420
DB 520 LLVAFAYLAAHFSVFEVFLDTLFLCFVAVDLTNDGSEKPYFMDPGFLSFVKRTDHF 579
QY 421 NNARAQDKHSLNREGTELOAIVR 445
DB 580 NNARSQGHKNSLPNEEGTELRPIVR 604

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RESULT 5
Q63ZS3_XENLA PRELIMINARY; PRT; 651 AA.
AC Q63ZS3;
DT 25-OCT-2004, integrated into UniProtKB/TrEMBL.
DT 25-OCT-2004, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE MGC82240 protein.
GN Name=MGC82240;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RA "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalon D.K., Murzyn D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Scherich A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RA Klein S., Gerhard D.S.;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
CC -----
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CC -----
DR EMBL; BC082837; AAH82837.1; -; mRNA.
DR InterPro; IPR007603; DUF580.
DR PANTHER; PTHR12385; DUF580; 1.
DR Pfam; PF04515; DUF580; 1.
SQ SEQUENCE 651 AA; 72937 MW; A26613B3055420AF CRC64;

Query Match 49.6%; Score 1147.5; DB 2; Length 651;
Best Local Similarity 49.6%; Pred. No. 3.8e-78;
Matches 221; Conservative 85; Mismatches 127; Indels 13; Gaps 4;

QY 1 MSGRDTILGICILALALSAMMFTFTITLLVHIFISVLGLFVCGVLMWLYDYTN 60
DB 205 MTSKEILMGCLLSVLMSLWITRIYTSRLVWITILVVLGSLGCTGVLMWLYADNKK 264
QY 61 DLS-----IELDTERENKCVLGFVAVSTGTVAVLLVIFVLRKRIKLTVELFQITNKAI 115

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Db 265 SLNENLPPDQLOVSKDNLQALLVVAIAATVETVILLMLLMRKRVALTIALENVAGKVF 324
Qy 116 SSAPFLFPQPLWTFATILFFVWLVAVLLSFTAGAAQVMEGGQVEYKPLSGIRYMSYH 175
Db 325 IHLPLLVFPQPTWTFALLFWVYVWVLLFLGTAGDPTNEQGFVERINGPLQYMWYH 384
Qy 176 LIGLIWTSFELACQOMTIAGAVTCTPNRSKNDPPDHPILSSLSILFFHQGVVKGSP 235
Db 385 LVGLIWSFELACQOMTIAGAVTCTPNRSKNDPPDHPILSSLSILFFHQGVVKGSP 235
Qy 236 LISVVRIPRIIVMYMGNALKEQOQHSRLNBEGETELQ 441
Db 445 IITLVKIPRIMLYIHSQKGEN-ACARCMLKSCICCLWCKLEKCLAYLNQAYTAIN 503
Qy 296 GTDFCTSAKDAPKILSKNSHFTSINCDFGDIIFLGLKVLVVCFTVFGMLAFNRAFOV 355
Db 504 STNFTCSAKDALVILVENALRVAAINTVGDPMFLGKILIVSCTGLAGIMLLNYQDYTV 563
Qy 356 WAVPLLLVAFYLVVAHSFSLVFTVLDALFLCFVADLETDGSGSEKPYFMDQEFSLFK 415
Db 564 WVLPLIIVCLFAFLVAHCFLSIYEMVVDVLFCLFAIDTKYNDGSPGKEFYMDKVLMEFVE 623
Qy 416 RSNKLNARAQODKHSRLNBEGETELQ 441
Db 624 DSR-----RALKEPGS--TAEGRELK 642

RESULT 6
O6IR74_XENLA
ID Q6IR74_XENLA PRELIMINARY; PRT; 651 AA.
AC Q6IR74;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 1.
DE MGC82240 protein.
GN Names=MGC82240;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uadin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U.,
RA Schnarch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Kidney;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
```

```
RT initiative.";
RL Dev. Dyn. 225:384-391 (2002).
[3]
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RA Klein S., Strausberg R.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
CC -----
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CC -----
DR EMBL: BC071026; AAH71026.1; -- mRNA.
DR InterPro: IPR007603; DUF580.
DR PANTHER: PTHR12385; DUF580; 1.
DR Pfam: PF04515; DUF580; 1.
SQ SEQUENCE 651 AA; 72908 MW; 619A2CB2C848FOAF CRC64;

Query Match 49.58; Score 1146.5; DB 2; Length 651;
Best Local Similarity 49.6%; Pred. No. 4.9e-78;
Matches 221; Conservative 85; Mismatches 127; Indels 13; Gaps 4;

Qy 1 MSGRDTILGLCILALALSLAMMTFTFRTITLLVHIFISLVILGLLFCVGLMWLYDYTN 60
Db 205 MTSKEIIMGLCLSLVLSMLMWIIRYISRVLWITILVVLGSLGTGVLWLYADNKK 264
Qy 61 DLS-----IELDTERENMKCVLGFIVSTGITAVLLVLFVLRKRIRKLTVELFOITNKA 115
Db 265 SLNENLPPDQLOVSKDNLQALLVVAIAATVETVILLMLLMRKRVALTIALENVAGKVF 324
Qy 116 SSAPFLFPQPLWTFATILFFVWLVAVLLSFTAGAAQVMEGGQVEYKPLSGIRYMSYH 175
Db 325 IHLPLLVFPQPTWTFALLFWVYVWVLLFLGTAGDPTNEQGFVERINGPLQYMWYH 384
Qy 176 LIGLIWTSFELACQOMTIAGAVTCTPNRSKNDPPDHPILSSLSILFFHQGVVKGSP 235
Db 385 LVGLIWSFELACQOMTIAGAVTCTPNRSKNDPPDHPILSSLSILFFHQGVVKGSP 235
Qy 236 LISVVRIPRIIVMYMGNALKEQOQHSRLNBEGETELQ 441
Db 445 IITLVKIPRIMLYIHSQKGEN-ACARCMLKSCICCLWCKLEKCLAYLNQAYTAIN 503
Qy 296 GTDFCTSAKDAPKILSKNSHFTSINCDFGDIIFLGLKVLVVCFTVFGMLAFNRAFOV 355
Db 504 STNFTCSAKDALVILVENALRVAAINTVGDPMFLGKILIVSCTGLAGIMLLNYQDYTV 563
Qy 356 WAVPLLLVAFYLVVAHSFSLVFTVLDALFLCFVADLETDGSGSEKPYFMDQEFSLFK 415
Db 564 WVLPLIIVCLFAFLVAHCFLSIYEMVVDVLFCLFAIDTKYNDGSPGKEFYMDKVLMEFVE 623
Qy 416 RSNKLNARAQODKHSRLNBEGETELQ 441
Db 624 DSR-----RALKEPGS--TAEGRELK 642

RESULT 7
CTL1 RAT
ID CTL1 RAT STANDARD; PRT; 656 AA.
AC Q8VJI6; Q9JUZ7;
DT 30-AUG-2005, integrated into UniProtKB/Swiss-Prot.
DT 01-MAR-2002, sequence version 1.
DT 07-MAR-2006, entry version 21.
DE Choline transporter-like protein 1 (Solute carrier family 44 member 1)
DE (CD92 antigen) (CDw92).
GN Names=Slc44a1; Synonyms=Cdw92, Ctl1;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 2), AND TISSUE SPECIFICITY.
RC TISSUE=Brain;
RX MEDLINE=20144127; PubMed=10677542; DOI=10.1073/pnas.030339697;
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RA O'Regan S., Traffort E., Ruat M., Cha N., Compaore D., Meunier F.-M.;
 RT "An electric lobe suppressor for a Yeast choline transport mutation
 RT belongs to a new family of transporter-like proteins.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:1835-1840(2000).
 [2]
 RN NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1), FUNCTION, AND TISSUE
 RP SPECIFICITY.
 RC STRAIN=Wistar; TISSUE=Brain;
 RX PubMed=15715662; DOI=10.1111/j.1471-4159.2004.02962.x;
 RA Traffort E., Ruat M., O'Regan S., Meunier F.-M.;
 RT "Molecular characterization of the family of choline transporter-like
 RT proteins and their splice variants.";
 RL J. Neurochem. 92:1116-1125(2005).
 [3]
 RN INDUCTION.
 RP PubMed=12007839; DOI=10.1016/S0169-328X(02)00182-1;
 RA Che Y.H., Yamashita T., Higuchi H., Tohyama M.;
 RT "Changes in mRNA for choline transporter-like protein following facial
 RT nerve transection.";
 RL Brain Res. Mol. Brain Res. 101:122-125(2002).
 [4]
 RN FUNCTION, AND TISSUE SPECIFICITY.
 RP PubMed=16000150; DOI=10.1111/j.1471-4159.2005.03299.x;
 RA Inazu M., Takeda H., Matsumiya T.;
 RT "Molecular and functional characterization of an Na-independent
 RT choline transporter in rat astrocytes.";
 RL J. Neurochem. 94:1427-1437(2005).
 [5]
 RN INDUCTION.
 RP PubMed=15691711; DOI=10.1016/j.mcn.2004.09.014;
 RA Leconte M.-J., De Gois S., Guerci A., Ravassard P., Faucon Biguet N.,
 RA Wallez J., Berrard S.;
 RT "Differential expression and regulation of the high-affinity choline
 RT transporter CHRI and choline acetyltransferase in neurons of superior
 RT cervical ganglia.";
 RL Mol. Cell. Neurosci. 28:303-313(2005).
 CC -I- FUNCTION: Probable choline transporter. May be involved in
 CC membrane synthesis and myelin production.
 CC -I- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein (By
 CC similarity).
 CC -I- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1; Synonyms=a;
 CC IsoId=Q8VII6-1; Sequence=Displayed;
 CC Name=2; Synonyms=b;
 CC IsoId=Q8VII6-2; Sequence=VSP_015429, VSP_015430;
 CC -I- TISSUE SPECIFICITY: Expressed in neurons, oligodendrocytes and
 CC astrocytes. Also expressed in the mucosal cell layer of the colon.
 CC -I- INDUCTION: By leukemia inhibitory factor or retinoic acid in
 CC vitro. In vivo, induced during the axonal elongation period
 CC following axotomy.
 CC -I- SIMILARITY: Belongs to the CTL (choline transporter-like) family.
 CC
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 CC
 CC -----
 CC ENBL; AJ245619; CAB75555.1; -; mRNA.
 CC ENBL; AJ240809; CAD12728.1; -; mRNA.
 CC Ensembl; ENSRNOG00000017846; Rattus norvegicus.
 CC RGD; 621426; Cdw92.
 CC InterPro; IPR007603; DUF580.
 CC PANTHER; PTHR12385; DUF580; 1.
 CC Pfam; PF04515; DUF580; 1.
 CC Alternative splicing; Membrane; Transmembrane; Transport.
 KW Choline transporter-like protein 1.
 FT CHAIN 1 656 /FTid=PRO_0000191714.
 FT
 FT TOPO_DOM 1 29 Cytoplasmic (Potential).
 FT TRANSMEM 30 50 Potential.
 FT TOPO_DOM 51 211 Extracellular (Potential).
 FT TRANSMEM 212 232 Potential.
 FT TOPO_DOM 233 237 Cytoplasmic (Potential).
 FT TRANSMEM 238 258 Potential.
 FT TOPO_DOM 259 287 Extracellular (Potential).
 FT

FT TRANSMEM 288 308 Potential.
 FT TOPO_DOM 309 314 Cytoplasmic (Potential).
 FT TRANSMEM 315 335 Potential.
 FT TOPO_DOM 336 337 Extracellular (Potential).
 FT TRANSMEM 338 358 Potential.
 FT TOPO_DOM 359 379 Cytoplasmic (Potential).
 FT TRANSMEM 380 400 Potential.
 FT TOPO_DOM 401 441 Extracellular (Potential).
 FT TRANSMEM 442 462 Potential.
 FT TOPO_DOM 463 536 Cytoplasmic (Potential).
 FT TRANSMEM 537 557 Potential.
 FT TOPO_DOM 558 585 Extracellular (Potential).
 FT TRANSMEM 586 586 Potential.
 FT TOPO_DOM 587 656 Cytoplasmic (Potential).
 FT COMPEIAS 473 491 Cys-rich.
 FT VARSPPLIC 650 653 /FTid=VSP_015429.
 FT
 FT VARSPPLIC 654 656 Missing (in isoform 2).
 FT
 FT CONFLICT 267 267 R -> S (in Ref. 1).
 FT CONFLICT 645 645 K -> E (in Ref. 1).
 FT
 FT SEQUENCE 656 AA; 73092 MW; 217AAD02F6E4D138 CRC64;
 SQ
 Query Match 48.9%; Score 1131; DB 1; Length 656;
 Best Local Similarity 50.0%; Pred. NO. 6.7e-77;
 Matches 212; Conservative 80; Mismatches 126; Indels 6; Gaps 2;
 QY 1 MSGRDTILGILALALSAMWTFRTTLAVHIFISVLVILGLFVCGVLWLYDYTN 60
 DB 208 MTSKEILGCLLSVLMSILMWIIRYISRVILWILTLVILGSLGGTGLWLYAKQR 267
 QY 61 D-----LSTELDERENMKCVLGFATVSTGTAIVLVILVILVLRKIKLTVELFOITNKAI 115
 DB 268 SPKETVPEQLQIAEDNLRALIYALSAVFTVILFLIMVLRKRVALTIALFHVAGKVF 327
 QY 116 SSAPFLLPQLMTFATLIFFWVLWVAVLSLGTAGAAQVMGGQVEYKPLSGIRYMWVSH 175
 DB 328 IHLPLLVFQPFWTFVALVFWAYIMTLFLGTGSAVQNEQGFVEYKISGPLQYMMWVH 387
 QY 176 LGLIWTSEFILLACQOMTIAGAVTCYFNRSKNDPDHPLSLSLTLFFVHOCTVVKGSF 235
 DB 388 VVGLIWISEFILLACQOMTVAGAVTVYTRDKRNLPTFILASVNRILIRYHLGTVAKGSF 447
 QY 236 LISVVRIPRIIYMYMONALKEQHGALSRYLFRCCYCCFWCLDKYLLHLNQNAYTTAIN 295
 DB 448 IITLVKIPRMILMYIHSQKGRN-ACARCMKSKICCLWCLCKLSYLNQAYTTAIN 506
 QY 296 GTDFCTSAKDAPKILSKNSHFTSINCPGDFIIFLGKLVVCFVTFGGLMAFNYNRAFOV 355
 DB 507 STNFTCTSAKDAFVILVENALRVAAINTVGDVFMFLFLGKVLIVCVSTGLAGIMLLNYQDDTV 566
 QY 356 WAVPLLLVAFVILVAHSFLSVFETVLDALFLCFVADLETDGSSSEKPYFMDQEFISFVK 415
 DB 567 WVLPLIIVCLFAPLVAHCFLSIYEMVVDVILFLCFALDTKINDSPGREFMVKVMEFVE 626
 QY 416 RSNK 419
 DB 627 NSRK 630
 RESULT 8
 CTL1_HUMAN STANDARD; PRT: 657 AA.
 ID CTL1_HUMAN Q9WUB3; Q9WUB3; Q9WUB3; Q9WUB3;
 AC Q9WUB3; Q9WUB3; Q9WUB3; Q9WUB3;
 DT 30-AUG-2005, integrated into UniProtKB/Swiss-Prot.
 DT 01-MAR-2002, sequence version 1.
 DT 07-MAR-2006, entry version 27.
 DE Choline transporter-like protein 1 (Solute carrier family 44 member 1)
 DE (CD92 antigen) (CDw92).
 DE Name=SLC44A1; Synonyms=CDW92, CTL1;
 GN Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND ALTERNATIVE SPLICING (ISOFORM 2).
 RC TISSUE=Ewing sarcoma;
 RX MEDLINE=2014127; PubMed=10677542; DOI=10.1073/pnas.03039697;
 RA O'Regan S., Traiffort E., Ruat M., Cha N., Compaore D., Meunier F.-M.;
 RT "An electric love suppressor for a yeast choline transport mutation
 belongs to a new family of transporter-like proteins.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:1835-1840(2000).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 3), AND TISSUE SPECIFICITY.
 RX MEDLINE=2155187; PubMed=11698453;
 RA Wille S., Sezeres A., Majdic O., Prager E., Staffler G., Stoeckl J.,
 RA Kunthaler D., Prieschl E.E., Baumrucker T., Burtscher H.,
 RA Zlabinger G.J., Knapp W., Stockinger H.;
 RT "Characterization of Cdw92 as a member of the choline transporter-like
 protein family regulated specifically on dendritic cells.";
 RL J. Immunol. 167:15795-15804(2001).
 RN [3]
 RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1).
 RC TISSUE=Ewing sarcoma;
 RX PubMed=15164053; DOI=10.1038/nature02465;
 RA Humphray S.J., Oliver K., Hunt A.R., Plumb R.W., Loveland J.E.,
 RA Howe K.L., Andrews T.D., Searle S., Hunt S.E., Scott C.B., Jones M.C.,
 RA Ainscough R., Almeida J.P., Ambrose K.D., Ashwell R.I.S.,
 RA Babbage A.K., Babbage S., Baguley C.L., Bailey J., Banerjee R.,
 RA Barker D.J., Barlow K.F., Bates K., Beasley H., Beasley O., Bird C.P.,
 RA Bray-Allen S., Brown A.J., Brown J.Y., Burford D., Burfill W.,
 RA Burton J., Carder C., Carter N.P., Chapman J.C., Chen Y., Clarke G.,
 RA Clark S.Y., Clee C.M., Clegg S., Collier R.E., Corby N., Crosier M.,
 RA Cummings A.T., Davies J., Dhani P., Dunn M., Dutta I., Dyer L.W.,
 RA Earthrow M.E., Faulkner L., Fleming C.J., Frankish A.,
 RA Frankland J.A., French L., Fricker D.G., Garner P., Garnett J.,
 RA Ghori J., Gilbert J.G.R., Gilson C., Grafham D.V., Gribble S.,
 RA Griffiths C., Griffiths-Jones S., Grocock R., Guy J., Hall R.E.,
 RA Hammond S., Harley J.L., Harrison E.S.I., Hart E.A., Heath P.D.,
 RA Henderson C.D., Hopkins B.L., Howard P.J., Howden P.J., Huckle E.,
 RA Johnson C., Johnson D., Joy A.A., Kay M., Keenan S., Kershaw J.K.,
 RA Kimberley A.M., King A., Knights A., Laird G.K., Langford C.,
 RA Lawlor S., Leongamornlert D.A., Leversha M., Lloyd C., Lloyd D.M.,
 RA Lovell J., Martin S., Mashreghi-Mohammadi M., Matthews L., McLaren S.,
 RA McLay K.E., McMurray A., Milne S., Nickerson T., Nisbett J.,
 RA Nordsiek G., Pearce A.V., Peck A.I., Porter K.M., Pandian R.,
 RA Peltan S., Phillimore B., Povey S., Ramsey Y., Rand V., Scharfe M.,
 RA Sehra H.K., Showkeen R., Sins S.K., Skuce C.D., Smith M.,
 RA Steward C.A., Swardbeck D., Sycamore N., Tester J., Thorpe A.,
 RA Tracey A., Tromans A., Thomas D.W., Wall M., Wallis J.M., West A.P.,
 RA Whitehead S.L., Willey D.L., Williams S.A., Wilming L., Wray P.W.,
 RA Young L., Ashurst J.L., Coulson A., Blocker H., Durbin R.,
 RA Sulston J.E., Hubbard T., Jackson M.J., Bentley D.R., Beck S.,
 RA Rogers J., Dunham I.;
 RT "DNA sequence and analysis of human chromosome 9.";
 RL Nature 429:369-374(2004).
 RN [5]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
 RC TISSUE=Eye, and Lung;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshlyuk S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abranson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Viallon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: Probable choline transporter. May be involved in
 membrane synthesis and myelin production (By similarity).
 CC -1- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein (By
 similarity).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=1; Synonyms=A;
 CC IsoId=Q8WW15-1; Sequence=Displayed;
 CC Name=2; Synonyms=B;
 CC IsoId=Q8WW15-2; Sequence=VSP_015424, VSP_015425;
 CC Name=3; Synonyms=C;
 CC IsoId=Q8WW15-3; Sequence=VSP_015426, VSP_015427;
 CC -1- TISSUE SPECIFICITY: Expressed in various cells of the
 hematopoietic system.
 CC -1- SIMILARITY: Belongs to the CTL (choline transporter-like) family.
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 DR EMBL; AJ275620; CAB75541.2; -; Genomic DNA.
 DR EMBL; AJ272365; CAC82175.1; -; mRNA.
 DR EMBL; AJ242812; CAD12764.1; -; Genomic DNA.
 DR EMBL; AL161627; CAI13069.1; JOINED; Genomic DNA.
 DR EMBL; AL450265; CAI13069.1; JOINED; Genomic DNA.
 DR EMBL; AL590368; CAI13069.1; JOINED; Genomic DNA.
 DR EMBL; AL161627; CAI13070.1; -; Genomic DNA.
 DR EMBL; AL450265; CAI13070.1; JOINED; Genomic DNA.
 DR EMBL; AL590368; CAI13070.1; JOINED; Genomic DNA.
 DR EMBL; AL161627; CAI13071.1; -; Genomic DNA.
 DR EMBL; AL450265; CAI13071.1; JOINED; Genomic DNA.
 DR EMBL; AL590368; CAI13071.1; JOINED; Genomic DNA.
 DR EMBL; AL450265; CAI14395.1; -; Genomic DNA.
 DR EMBL; AL161627; CAI14395.1; JOINED; Genomic DNA.
 DR EMBL; AL590368; CAI14395.1; JOINED; Genomic DNA.
 DR EMBL; AL450265; CAI14395.1; JOINED; Genomic DNA.
 DR EMBL; AL161627; CAI14396.1; -; Genomic DNA.
 DR EMBL; AL450265; CAI14396.1; JOINED; Genomic DNA.
 DR EMBL; AL590368; CAI14396.1; JOINED; Genomic DNA.
 DR EMBL; AL450265; CAI14397.1; -; Genomic DNA.
 DR EMBL; AL161627; CAI14397.1; JOINED; Genomic DNA.
 DR EMBL; AL590368; CAI14397.1; JOINED; Genomic DNA.
 DR EMBL; AL450265; CAH73434.1; -; Genomic DNA.
 DR EMBL; AL161627; CAH73434.1; JOINED; Genomic DNA.
 DR EMBL; AL590368; CAH73434.1; JOINED; Genomic DNA.
 DR EMBL; AL450265; CAH73435.1; -; Genomic DNA.
 DR EMBL; AL161627; CAH73435.1; JOINED; Genomic DNA.
 DR EMBL; AL450265; CAH73435.1; JOINED; Genomic DNA.
 DR EMBL; AL590368; CAH73436.1; -; Genomic DNA.
 DR EMBL; AL161627; CAH73436.1; JOINED; Genomic DNA.
 DR EMBL; AL450265; CAH73436.1; JOINED; Genomic DNA.
 DR EMBL; BC018213; AAH18213.1; -; mRNA.
 DR EMBL; BC049203; AAH49203.1; -; mRNA.
 DR Ensembl; ENSG00000070214; Homo sapiens.
 DR HGNC; HGNC:18798; SLC44A1.
 DR MIM; 606105; gene.
 DR InterPro; IPR007603; DUF580.
 DR PANTHER; PTHR12385; DUF580; 1.
 DR Pfam; PF04515; DUF580; 1.
 KW Alternative splicing; Antigen; Membrane; Transmembrane; Transport.
 FT CHAIN 1 657 /FTid=PRO_0000191712.

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FT TOPO_DOM 1 30 Cytoplasmic (Potential).
FT TRANSMEM 31 51 Potential.
FT TOPO_DOM 52 212 Extracellular (Potential).
FT TRANSMEM 213 233 Potential.
FT TOPO_DOM 234 238 Cytoplasmic (Potential).
FT TRANSMEM 239 259 Potential.
FT TOPO_DOM 260 288 Extracellular (Potential).
FT TRANSMEM 289 309 Potential.
FT TOPO_DOM 310 315 Cytoplasmic (Potential).
FT TRANSMEM 316 336 Potential.
FT TOPO_DOM 337 338 Extracellular (Potential).
FT TRANSMEM 339 359 Potential.
FT TOPO_DOM 360 380 Cytoplasmic (Potential).
FT TRANSMEM 381 401 Potential.
FT TOPO_DOM 402 442 Extracellular (Potential).
FT TRANSMEM 443 463 Potential.
FT TOPO_DOM 464 537 Cytoplasmic (Potential).
FT TRANSMEM 538 558 Potential.
FT TOPO_DOM 559 566 Extracellular (Potential).
FT TRANSMEM 567 587 Potential.
FT TOPO_DOM 588 657 Cytoplasmic (Potential).
FT COMPIAS 651 492 Cys-rich.
FT VARSPLIC 651 652 ASGA -> LKKR (in isoform 2).
FT 652 AS -> IK (in isoform 3).
FT 653 Missing (in isoform 3).
FT VARSPLIC 653 657 /FTId=VSP_015426.
FT 655 Missing (in isoform 2).
FT VARSPLIC 655 657 /FTId=VSP_015425.
FT 79 79 I -> V (in Ref. 2).
FT CONFLICT 644 644 S -> A (in Ref. 2).
SQ SEQUENCE 657 AA; 73302 MW; 10D70CAB8E33E3AC CRC64;

Query Match 48.4%; Score 1121; DB 1; Length 657;
Best Local Similarity 49.8%; Pred. No. 3.8e-76;
Matches 211; Conservative 80; Mismatches 127; Indels 6; Gaps 2;

QY 1 MSGRDILGCIALLALSLAMMTFFRITLLVHIFSLVILGLFVCGVLWLYDYTN 60
DB 209 MTSKEILGICLLSLMSILMVIIRYISRVLMVILTLVILSGLOGTGVLWLYAKQR 268
QY 61 D-----LSIELDTERENMKCVGFAIVSTGITAVLLVLFVLKRKIKLTVELFOITNKAI 115
DB 269 SPKETVTEQLOIAEDNLRALLIYASATVFTVILFLIMLVMRKRVALLTIALFHVAGKVF 328
QY 116 SSAPFLLPQPLWTFAILIFFFWLWVAVLLSLGTAGAAQVMGQVEYKPLSGIRYMSYH 175
DB 329 IHLPLLVFPQFTFFALVLEFWYVIMTLLFLGTGSPVQNEQGFVEFKISGPLQYMWYH 388
QY 176 LIGLIWTSFETLACQMTIAGAVVTCYFNRSKNDPPDHPILSLISLILFFVHOGTVVKGSP 235
DB 389 VGLIWISEFILACQMTVAGAVVTVYFTDRKNLPPTPILASVNLRIYVHLGTVAKGSP 448
QY 236 LISVRIPIRIVVMONALKEOQHGLSRYLFRCCYCCFWCLDKYLHLNQNAYTTAIN 295
DB 449 IITLVKIPRIMLYIHSQKGEN-ACARCVLSKSCICLWCLKNLYLNQAYTATIN 507
QY 296 GTDFCTSAKDAFKILSKNSHFTSINGFGDFIIFLGKVLVVCFTVFGGLMAFNNRAFOV 355
DB 508 STNFTSAKDAFVLVNALRVATINTVGDGFMFLFGKVLIVCSTGLAGIMLLNQDYTV 567
QY 356 WAPVLLLVAFVILVAHSFLSVETVLDALFLCAVDLENTDGSSEKPYFMDOEFLSFVK 415
DB 568 WVLPIIIVCLVAFVLAHCFSLSIEMVVDVFLCAIDTKYNDGSPGREFTYNDKVLMEFVE 627
QY 416 RSNK 419
DB 628 NSRK 631
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RESULT 9

CTL1_TORMA

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ID AC Q919B9; CTL1_TORMA STANDARD; PRT; 646 AA.
DT 30-AUG-2005, integrated into UniProtKB/Swiss-Prot.
DT 01-OCT-2000, sequence version 1.
DT 07-FEB-2006, entry version 17.
DE Choline transporter-like protein 1.
GN Name=CTL1;
OS Torpedo marmorata (Marbled electric ray).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squalea; Hynostomalea; Pristigaster, Batoidea,
OC Torpediniformes; Torpedinidae; Torpedinidae; Torpedo.
OX NCBI_TaxID=7788;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA], AND FUNCTION.
RX MEDLINE=20144127; PubMed=10677542; DOI=10.1073/pnas.030339697;
RA O'Regan S., Traiffort E., Ruat M., Cha N., Compaore D., Meunier F.-M.;
RT 'An electric lobe suppressor for a yeast choline transporter mutation
RT belongs to a new family of transporter-like proteins.';
RN Proc. Natl. Acad. Sci. U.S.A. 97:1835-1840(2000).
RL [2]
RP TISSUE SPECIFICITY, AND SUBCELLULAR LOCATION.
RX PubMed=12352613; DOI=10.1097/00001756-200209160-00009;
RA Meunier F.-M., O'Regan S.;
RT 'Expression of CTL1 in myelinating structures of Torpedo marmorata.';
RN NeuroReport 13:1617-1620(2002).
RP [3]
RP FUNCTION, AND TISSUE SPECIFICITY.
RX PubMed=12675144; DOI=10.1023/A:1022877524469;
RA O'Regan S., Meunier F.-M.;
RT 'Selection and characterization of the choline transporter mutation
RT suppressor from Torpedo electric lobe, CTL1.';
RN Neurochem. Res. 28:551-555(2003).
RL CC -!- FUNCTION: Probable choline transporter. May be involved in
CC membrane synthesis and myelin production.
CC -!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein.
CC -!- TISSUE SPECIFICITY: Present in myelinated structures from brain
CC and spinal chord (at protein level).
CC -!- SIMILARITY: Belongs to the CTL (choline transporter-like) family.
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CC -----
DR EMBL; AJ245618; CAB75556.1; -; mRNA.
DR InterPro; IPR007603; DUF580.
DR PANTHER; PTHR12385; DUF580; 1.
DR Pfam; PF04515; DUF580; 1.
KW Membrane; Transmembrane; Transport.
FT CHAIN 1 646 Choline transporter-like protein 1.
FT TOPO_DOM 1 27 Cytoplasmic (Potential).
FT TRANSMEM 28 48 Potential.
FT TOPO_DOM 49 207 Extracellular (Potential).
FT TRANSMEM 208 228 Potential.
FT TOPO_DOM 229 233 Cytoplasmic (Potential).
FT TRANSMEM 234 254 Potential.
FT TOPO_DOM 255 281 Extracellular (Potential).
FT TRANSMEM 282 302 Potential.
FT TOPO_DOM 303 308 Cytoplasmic (Potential).
FT TRANSMEM 309 329 Potential.
FT TOPO_DOM 330 331 Extracellular (Potential).
FT TRANSMEM 332 352 Potential.
FT TOPO_DOM 353 373 Cytoplasmic (Potential).
FT TRANSMEM 374 394 Potential.
FT TOPO_DOM 395 435 Extracellular (Potential).
FT TRANSMEM 436 456 Potential.
FT TOPO_DOM 457 530 Cytoplasmic (Potential).
FT TRANSMEM 531 551 Potential.
FT TOPO_DOM 552 559 Extracellular (Potential).
FT TRANSMEM 560 580 Potential.
FT TOPO_DOM 581 646 Cytoplasmic (Potential).
FT COMPIAS 467 485 Cys-rich.
SQ SEQUENCE 646 AA; 72254 MW; A19A0E1D81453F6F CRC64;
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Query Match 48.2%; Score 1116; DB 1; Length 646;
Best Local Similarity 48.3%; Pred. No. 9e-76;
Matches 204; Conservative 89; Mismatches 125; Indels 4; Gaps 2;

QY 1 MSGRTDILGICILALSLAMMFTFRITLLVHIFISLVILGLFVCGVLMWLYDYDTN 60
DB 204 MTSKEIIVGLCLSVLSILMLWIRYISKVWILAILIIGSIGTAVLWMLYADHKK 263
QY 61 DLSIEL---DTERENKCVLGFPAIVSGITAVLVLVFLVLRKRIKLVFELQITNKAISS 117
DB 264 TLKLDPSQGVADNVNTALLVCAIIATVITVILLMLINKRKRVALTIALFHVAGKVFH 323
QY 118 APFLFLOPIATFALLIFPFWLWAVLISLGTAGNAQWMEGVYKPLSGIRYMWVHLI 177
DB 324 IPELIFOSLWTFALAFWYIAVLVLLATAGYPOKKDQGYVEFKVSGPLQVTWYHLV 383
QY 178 GLIWTSEFILAQQMTITAGAVTTCYFNRSKNDPDHPIILSLSLFFPHOGTVKGSFLI 237
DB 384 GLIWISEFILAQQMTITAGAVTTCYFNRSKNDPDHPIILSLSLFFPHOGTVKGSFLI 443
QY 238 SVVRIPRIIVYMONALKEQHQGALSRFLPCYCCFWCLDKYLLHLNQNAYTTTAINGT 297
DB 444 TLIKIPQMLVYIHSQKGRN-ACAKMLKACWCLWCKLEKCLLYLRNAYIATSINGT 502
QY 298 DPTCSAKDAFKILSKNSHTSFNCFDGFIFIGKVLVVCFTVFGGLMAFNARAFQVWA 357
DB 503 SFCTSAKDAIVLVENARVAANTVGDVFLFKLILVLTGFGVGIILLNYORDYTVWV 562
QY 358 VPILLVAFPAVLVAHSLFSLVFETVLDAFLFCFVADLTNDGSSSEKPKVFMDOEFLSVKRS 417
DB 563 LPIIICLFAFFVSHCFSLSIYMWVVDVFLFCFVADCKHNDGSPGREYIMDKSLMEFMD 622
QY 418 NK 419
DB 623 RK 624

RESULT 10
CTLI MOUSE
ID CTLI1 MOUSE STANDARD; PRT; 653 AA.
AC Q6X893; Q6X894; Q91229;
DT 30-AUG-2005, integrated into UniProtKB/Swiss-Prot.
DT 07-MAR-2006, sequence version 2.
DE Choline transporter-like protein 1 (Solute carrier family 44 member 1)
DE (CD92 antigen) (CDw92).
GN Name=Slc44a1; Synonyms=Cdw92, Ctl1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS 1 AND 2), TISSUE SPECIFICITY,
RP SUBCELLULAR LOCATION, AND FUNCTION.
RC TISSUE=Brain;
RA Yuan Z., Wagner L., Polomienko A., Bakovic M.;
RA PubMed=15474312; DOI=10.1016/j.j.gene.2004.07.042;
RT "Identification and expression of a mouse muscle-specific CTL1 gene."
RL Gene 341:305-312(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 390-653 (ISOFORM 1).
RP STRAIN=FVB/N; TISSUE=Liver, and Mammary gland;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins L., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Sapatton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
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Query Match

48.1%; Score 1113; DB 1; Length 653;

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RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting J., Helton E., Kettaman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buttrick Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnur A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC - FUNCTION: Probable choline transporter. May be involved in
CC membrane synthesis and myelin production.
CC - SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein.
CC - ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1; Synonyms=A;
CC IsoId=Q6X893-1; Sequence=Displayed;
CC Name=2; Synonyms=B;
CC IsoId=Q6X893-2; Sequence=VSP_015428;
CC - TISSUE SPECIFICITY: Specifically abundant in skeletal muscle (at
CC protein level).
CC - SIMILARITY: Belongs to the CTL (choline transporter-like) family.
CC
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CC -----
DR ENBL; AY249865; AAP81042.1; -; mRNA.
DR ENBL; AY249866; AAP81043.1; -; mRNA.
DR ENBL; BC010258; AAH10258.1; -; mRNA.
DR ENBL; BC025941; AAH25941.1; ALT_INIT; mRNA.
DR Ensembl; ENSMUSG0000028412; Mus musculus.
DR MGI; MGI:2140592; Slc44a1.
DR GO; GO:0016021; C:integral to membrane; IDA.
DR GO; GO:0015220; F:choline transporter activity; IDA.
DR GO; GO:0015871; P:choline transport; IDA.
DR InterPro; IPR007603; DUF580.
DR Pfam; PF04515; DUF580; 1.
KW Alternative splicing; Membrane; Transmembrane; Transport.
CHAIN 1 653
FT TOPO_DOM 1 29
FT TRANSMEM 30 50
FT TOPO_DOM 51 211
FT TRANSMEM 212 232
FT TOPO_DOM 233 237
FT TRANSMEM 238 258
FT TOPO_DOM 259 287
FT TRANSMEM 288 308
FT TOPO_DOM 309 314
FT TRANSMEM 315 335
FT TOPO_DOM 336 337
FT TRANSMEM 338 358
FT TOPO_DOM 359 379
FT TRANSMEM 380 400
FT TOPO_DOM 401 441
FT TRANSMEM 442 462
FT TOPO_DOM 463 536
FT TRANSMEM 537 557
FT TOPO_DOM 558 565
FT TRANSMEM 566 586
FT TOPO_DOM 587 653
FT COMPTIAS 473 491
FT VARSPPLIC 650 653
FT
FT CONFLICT 426 426
FT CONFLICT 439 439
FT CONFLICT 510 510
FT SEQUENCE 653 AA; 73083 MW; 3857DA8BE428EFF5 CRC64;
SQ

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DR Pfam; PF04515; DUF580; 1.
SQ SEQUENCE 691 AA; 7608 MW; 0BBF06C93F0A3EA0 CRC64;

Query Match 27.0%; Score 624.5; DB 2; Length 691;
Best Local Similarity 31.7%; Pred. No. 1.3e-38;
Matches 136; Conservative 81; Mismatches 169; Indels 43; Gaps 4

Qy 10 LCIALALSLAMMTFFRITTLVHIFISLVILGLLFCVGVLMWLYDYDTNDLSIE---- 65
Db 211 VCGLLALISIALVTMMHLSRIVSWIIICVLIVIVASVALTVWALYAYYINIRKSGVNTQYS 270
Qy 66 -LDTERENMKCVLGFVAVSTGITAVLLVLLFVLRKRIKLTVELFQITNKAISSAPFLLFQ 124
Db 271 MLEEFVRNQAVLTLAVLATITMLILVVIYFLKNKLAGLSALFEEAGCCMMNLPGLLIA 330
Qy 125 PLMTFAILIPFWLWVAVLLSLGTAGAA----- 152
Db 331 PLLAFLVLI AFLSPFVAIIICLATATSPGQSPIAFDNSKAHQQLPANALFVSNSTDVN 390
Qy 153 QVMGGQVEYKPLSGIRYMSYHLIGLITSEPTLACQOMTIAGAVVTCYNRKNDDPPD 212
Db 391 DLARNARVEYADAGVLRSMFWIYVVGILWITVEFIFACQFALAAVAFWYFQK----PTS 446
Qy 213 HPILSSLSLFFHYHOGVNVKSGSLISVVVRPIRIWVMYQNALK--EQOHGALSRYLPRCC 270
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Db 507 ICGFWLLEKIFRLNHNAYTVVALESINFCPAGAIANNAMATNVLOVATINSVGFILFL 566
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DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DT 21-FEB-2006, entry version 20.
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GN Name=CG1311; ORFNames=Dmel_CG1311;
OS Drosophila melanogaster (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxId=7227;
RN R1
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RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Neilson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*";
 Science 287:2195-2195(2000).
 RN [2]
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 RN NUCLEOTIDE SEQUENCE.
 RP MEDLINE=22426065; PubMed=12537568;
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 RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
 RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
 RA Pacleb J.M., Park S., Pfeiffer B.B., Richards S., Sodergren E.J.,
 RA Svirskas R., Taber P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
 RT "Finishing a whole-genome shotgun: release 3 of the *Drosophila*
 RT melanogaster euchromatic genome sequence.";
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
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 RP MEDLINE=22426070; PubMed=12537573;
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 RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R.,
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celniker S.E.;
 RT "The transposable elements of the *Drosophila melanogaster* euchromatin:
 RT a genomics perspective.";
 RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
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 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Battencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
 RT systematic review";
 RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
 RN [5]
 RN
 RN NUCLEOTIDE SEQUENCE.
 RP Berkeley *Drosophila* Genome Project;
 RG Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
 RA Hoskins R., Stapleton J., Pacleb J., Park S., Svirskas R., Smith E.,
 RA Yu C., Rubin G.;
 RT "Drosophila melanogaster release 4 sequence";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RN
 RN NUCLEOTIDE SEQUENCE.
 RP FlyBase;
 RG
 RN
 RN Submitted (JAN-2006) to the EMBL/GenBank/DBJ databases.
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 CC
 CC EMBL: AE003480; AAF47876.1; -; Genomic DNA.

DR	FlyBase; FBgn0035523; CG1311.
DR	InterPro; IPR007603; DUF580.
DR	PANTHER; PTHR12385; DUF580; 1.
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Matches 136; Conservative	81; Mismatches 169; Indels 43; Gaps 4
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QY	66 -LDTERENMKCVLGFAIVSTGITAALLVLFLVLRKRKLTVELFOITNKAISSAPFLLFQ 124
DB	271 MLEEFVENQAULTAVLATITMIILVIWIYFLKNLAGLSALFEEAGOCMNNLPGLLIA 330
QY	125 PLMTFPAILIFFWULWVAVLLSLGTAGA-----
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DT	19-JUL-2004, integrated into UniProtKB/TREMBL.
DT	19-JUL-2004, sequence version 1.
DT	07-FEB-2006, entry version 12.
DE	MGC83045 protein.
GN	Name=MGC83045;
OS	Xenopus laevis (African clawed frog).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC	Xenopodinae; Xenopus; Xenopus.
OX	NCB_I_TaxID=8355;
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RC	TISSUE=Embryo;
RC	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA	Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA	Stauberg R.D., Collins F.S., Wagner L., Shermen C.M., Schuler G.D.,
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.J., Hsieh P.,
RA	Diatchenko L., Marinisa K., Farmer A.A., Rubin G.W., Hong L.,
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA	Brownstein M.J., Usdin T.B., Tohiyuki S., Carninci P., Prange C.,
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA	Villalon D.K., Muzny D.M., Sodergren E.U., Lu X., Gibbs R.A.,
RA	Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

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OM protein - protein search, using sw model

Run on: June 6, 2006, 22:03:21 ; Search time 51 Seconds
(without alignments)
763.748 Million cell updates/sec

Title: US-10-063-537-32

Perfect score: 2315

Sequence: 1 MSGRDTILGLCILALSLA.....QQDKHSLRNEGTQLQAIR 445

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /EMC_Celerra_SID3S/ptodata/2/iaa/5_COMB.pep.*
- 2: /EMC_Celerra_SID3S/ptodata/2/iaa/6_COMB.pep.*
- 3: /EMC_Celerra_SID3S/ptodata/2/iaa/7_COMB.pep.*
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- 5: /EMC_Celerra_SID3S/ptodata/2/iaa/PTUS_COMB.pep.*
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- 7: /EMC_Celerra_SID3S/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2315	100.0	445	2	US-09-991-181-177
2	2315	100.0	445	2	US-09-990-444-177
3	2315	100.0	445	2	US-09-997-333-177
4	2315	100.0	445	2	US-09-992-598-177
5	2315	100.0	445	2	US-09-989-735-177
6	2315	100.0	445	3	US-09-989-726-177
7	2315	100.0	445	3	US-09-997-514-177
8	2315	100.0	445	3	US-09-989-728-177
9	2315	100.0	445	3	US-09-997-349-177
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13	563	24.3	717	2	US-10-104-047-3465
14	540	23.3	710	2	US-09-547-789-2
15	538.5	23.3	705	2	US-09-547-789-5
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21	428	18.5	321	2	US-09-989-735-36
22	428	18.5	321	3	US-09-989-726-36
23	428	18.5	321	3	US-09-997-514-36
24	428	18.5	321	3	US-09-989-728-36
25	428	18.5	321	3	US-09-997-349-36
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ALIGNMENTS

RESULT 1

US-09-991-181-177

; Sequence 177, Application US/09991181

; Patent No. 6913919

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE REFERENCE: P27301C53

; CURRENT APPLICATION NUMBER: US/09/991,181

; CURRENT FILING DATE: 2001-11-16

; PRIOR APPLICATION NUMBER: 60/049787

; PRIOR FILING DATE: 1997-06-16

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/065186

; PRIOR FILING DATE: 1997-11-12

; PRIOR APPLICATION NUMBER: 60/065311

; PRIOR FILING DATE: 1997-11-13

; PRIOR APPLICATION NUMBER: 60/066770

; PRIOR FILING DATE: 1997-11-24

; PRIOR APPLICATION NUMBER: 60/075945

; PRIOR FILING DATE: 1998-02-25

; PRIOR APPLICATION NUMBER: 60/078910

; PRIOR FILING DATE: 1998-03-20

; PRIOR APPLICATION NUMBER: 60/083322

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Sequence 21, Appl
Sequence 741, App
Sequence 166, App
Sequence 166, App
Sequence 4684, Ap
Sequence 46, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 2, Appli
Sequence 5, Appli
Sequence 46, Appl
Sequence 10, Appl
Sequence 342, App
Sequence 5, Appli
Sequence 3, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 6, Appli

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2	PRIOR FILING DATE: 1998-06-17
3	PRIOR APPLICATION NUMBER: 60/089653
4	PRIOR FILING DATE: 1998-06-17
5	PRIOR APPLICATION NUMBER: 60/089801
6	PRIOR FILING DATE: 1998-06-18
7	PRIOR APPLICATION NUMBER: 60/089907
8	PRIOR FILING DATE: 1998-06-18
9	PRIOR APPLICATION NUMBER: 60/089908
10	PRIOR FILING DATE: 1998-06-18
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13	PRIOR APPLICATION NUMBER: 60/089948
14	PRIOR FILING DATE: 1998-06-19
15	PRIOR APPLICATION NUMBER: 60/089952
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63	PRIOR APPLICATION NUMBER: 60/091360
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65	PRIOR APPLICATION NUMBER: 60/091478
66	PRIOR FILING DATE: 1998-07-02
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69	PRIOR APPLICATION NUMBER: 60/091519
70	PRIOR FILING DATE: 1998-07-02
71	PRIOR APPLICATION NUMBER: 60/091626
72	PRIOR FILING DATE: 1998-07-02
73	PRIOR APPLICATION NUMBER: 60/091633


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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

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Db 421 NNARAOQDKSLRNEEGTELQAIVR 445

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; Sequence 177, Application US/09990444
; Patent No. 6930170
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
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; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 2315; DB 2; Length 445;
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Db	181	WTSEFILACQOMTIAGAVVTCYFNRSKNDDPPHPIILSSLSILFFYHQGTWVKGSLISVV	240
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; Sequence 177, Application US/09997333
; Patent No. 6953836
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David
APPLICANT: Deenoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C27
CURRENT APPLICATION NUMBER: US/09/997,333
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RESULT 4

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; APPLICANT: Zhang, Zemin
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52	PRIOR FILING DATE: 1998-07-01
53	PRIOR APPLICATION NUMBER: 60/091360
54	PRIOR FILING DATE: 1998-07-01
55	PRIOR APPLICATION NUMBER: 60/091478
56	PRIOR FILING DATE: 1998-07-02
57	PRIOR APPLICATION NUMBER: 60/091544
58	PRIOR FILING DATE: 1998-07-01
59	PRIOR APPLICATION NUMBER: 60/091519
60	PRIOR FILING DATE: 1998-07-02
61	PRIOR APPLICATION NUMBER: 60/091626
62	PRIOR FILING DATE: 1998-07-02
63	PRIOR APPLICATION NUMBER: 60/091633
64	PRIOR FILING DATE: 1998-07-02
65	PRIOR APPLICATION NUMBER: 60/091978
66	PRIOR FILING DATE: 1998-07-07
67	PRIOR APPLICATION NUMBER: 60/091982
68	PRIOR FILING DATE: 1998-07-07
69	PRIOR APPLICATION NUMBER: 60/092182
70	PRIOR FILING DATE: 1998-07-09

Query Match	100.0%;	Score 2315;	DB 2;	Length 445;
Best Local Similarity	100.0%;	Pred. No. 1.9e-241;		

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Db 61 DLSIELDTRENNKCVLGFVAIVSTGITAVALLVLFVLRKRIKLTVELFOITNKKAISSAPF 120
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Db 121 LLFQPLWTFAILFFWVWVAVLLSGTAGAAQVMEGGQVEYKPLSGIRYMWSYHLIGLI 180
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Db 241 RPIRIIWMYQNALKEQOHGALSRYLFRCCYCCFWCLDKYLLHLNQNAVYTTTAINGTDFC 300
QY 301 TSAKDAFKILSKNSSHTSINCFGDFIIFLGKVLVVCFTVFGGLMAFNYNRAFQVWAVPL 360
Db 301 TSAKDAFKILSKNSSHTSINCFGDFIIFLGKVLVVCFTVFGGLMAFNYNRAFQVWAVPL 360
QY 361 LLVAFAYLVAHSLVFFETVLDALFLCFVADLETNDGSEKPYFMDQEFLSFVKBSNKL 420
Db 361 LLVAFAYLVAHSLVFFETVLDALFLCFVADLETNDGSEKPYFMDQEFLSFVKBSNKL 420
QY 421 NNAAQODKHSLSNEEGTELOAIVR 445
Db 421 NNAAQODKHSLSNEEGTELOAIVR 445

RESULT 5
US-09-989-735-177
; Sequence 177, Application US/09989735
; Patent No. 6972185
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1G61
; CURRENT APPLICATION NUMBER: US/09/989,735
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: 60/089440
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089512
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; PRIOR FILING DATE: 1998-06-16
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; PRIOR FILING DATE: 1998-06-26

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; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091778
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 2315; DB 2; Length 445;
Best Local Similarity 100.0%; Pred. No. 1.9e-241;
Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 121 LFPQPLWTFAILFFFWLVWVAVLLSLGTAGAAQMEGGQVEYKPLSGIRYMWVHLLGLI 180
Db 121 LFPQPLWTFAILFFFWLVWVAVLLSLGTAGAAQMEGGQVEYKPLSGIRYMWVHLLGLI 180

Qy 181 WTSEFILACQOMTIAGAVTTCYENRKNDDPPDHPILSSLSILFFYHOGTVVKGSLISVV 240
Db 181 WTSEFILACQOMTIAGAVTTCYENRKNDDPPDHPILSSLSILFFYHOGTVVKGSLISVV 240

Qy 241 RIPRIIWMYQNALKEQHGALSRYLFRCCYCCFWCLDKYLLHLNQNAYTTTAINGTDFC 300
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Qy 301 TSAKDAFKILSKNSHFTSINCFDPIIFLGKLVVVCFTVFGGLMAFNRAFOVWAVPL 360
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Qy 361 LLVAFAYLVVHSLVSVFETVLDALFLCPAVDLETNDGSSEKPYFMDQEFLSFVKRSNKL 420
Db 361 LLVAFAYLVVHSLVSVFETVLDALFLCPAVDLETNDGSSEKPYFMDQEFLSFVKRSNKL 420

Qy 421 NNARAQODKHSRNEEGTELQAIVR 445
Db 421 NNARAQODKHSRNEEGTELQAIVR 445

RESULT 6
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; Sequence 177, Application US/09989726
; Patent No. 7018811
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.	PRIOR APPLICATION NUMBER: 60/088730
APPLICANT: Kijavini, Ivar J.	PRIOR FILING DATE: 1998-06-10
APPLICANT: Napier, Mary A.	PRIOR APPLICATION NUMBER: 60/088742
APPLICANT: Pan, James	PRIOR FILING DATE: 1998-06-10
APPLICANT: Paoni, Nicholas F.	PRIOR APPLICATION NUMBER: 60/088810
APPLICANT: Roy, Margaret Ann	PRIOR FILING DATE: 1998-06-10
APPLICANT: Stewart, Timothy A.	PRIOR APPLICATION NUMBER: 60/088824
APPLICANT: Tumas, Daniel	PRIOR FILING DATE: 1998-06-10
APPLICANT: Watanabe, Colin K.	PRIOR APPLICATION NUMBER: 60/088826
APPLICANT: Williams, P. Mickey	PRIOR FILING DATE: 1998-06-10
APPLICANT: Wood, William I.	PRIOR APPLICATION NUMBER: 60/088858
APPLICANT: Zhang, Zemin	PRIOR FILING DATE: 1998-06-11
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic	PRIOR APPLICATION NUMBER: 60/088861
TITLE OF INVENTION: Acids Encoding the Same	PRIOR FILING DATE: 1998-06-11
FILE REFERENCE: P2730P1C60	PRIOR APPLICATION NUMBER: 60/088876
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PRIOR APPLICATION NUMBER: 60/062250	PRIOR FILING DATE: 1998-06-16
PRIOR FILING DATE: 1997-10-17	PRIOR APPLICATION NUMBER: 60/089512
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PRIOR APPLICATION NUMBER: 60/088217	PRIOR FILING DATE: 1998-06-24
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PRIOR APPLICATION NUMBER: 60/088655	PRIOR FILING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-09	PRIOR APPLICATION NUMBER: 60/090535
PRIOR APPLICATION NUMBER: 60/088734	PRIOR FILING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-10	PRIOR APPLICATION NUMBER: 60/090540

1 PRIOR FILING DATE: 1998-06-24
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7 PRIOR FILING DATE: 1998-06-25
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21 PRIOR FILING DATE: 1998-06-26
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23 PRIOR FILING DATE: 1998-07-01
24 PRIOR APPLICATION NUMBER: 60/091478
25 PRIOR FILING DATE: 1998-07-02
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33 PRIOR FILING DATE: 1998-07-02
34 PRIOR APPLICATION NUMBER: 60/091978
35 PRIOR FILING DATE: 1998-07-07
36 PRIOR APPLICATION NUMBER: 60/091982
37 PRIOR FILING DATE: 1998-07-07
38 PRIOR APPLICATION NUMBER: 60/092182
39 PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 2315; DB 3; Length 445;
Best Local Similarity 100.0%; Pred. No. 1.9e-241; Mismatches 0; Indels 0; Gaps 0;
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DB 121 LLFQPLMTFAILLFFVWLWAVLLSLCTAGAAQWMEGGQVEYKPLSGIRYVWWSYHLIGLI 180
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DB 181 WTSEFILACQMTIAGAVVTCYFNRSKNDPPDHPILSSLSILFFYHQTGVVKSFLISVV 240
QY 241 RPIRIIWMQNALKEQHGALSRYLPRCCYCCFWCLDKYLLHLNQNAVYTTTAINGTDFC 300
DB 241 RPIRIIWMQNALKEQHGALSRYLPRCCYCCFWCLDKYLLHLNQNAVYTTTAINGTDFC 300
QY 301 TSADAPKILSKNSHSTSNCGDFIIFLGKVLVVCFTVFGGLMAFNYNRAQVMAVPL 360
DB 301 TSADAPKILSKNSHSTSNCGDFIIFLGKVLVVCFTVFGGLMAFNYNRAQVMAVPL 360
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DB 361 LLVAFFAYLVHAFSLVSFVETVLDALFLCFAVDLETNDGSSSEKPYFMDQEFSLFVKRSNKL 420
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DB 421 NNARAQODKHSRLNEEGTELQAIVR 445
RESULT 7
US-09-997-514-177
; Sequence 177, Application US/09997514
; Patent No. 7019116
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deanoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
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; APPLICANT: Napier, Mary A.
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; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Maranabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C46
; CURRENT APPLICATION NUMBER: US/09/997,514
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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; PRIOR FILING DATE: 1997-10-17
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57	PRIOR APPLICATION NUMBER: 60/091982
58	PRIOR FILING DATE: 1998-07-07
59	PRIOR APPLICATION NUMBER: 60/092182
60	PRIOR FILING DATE: 1998-07-09

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; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
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; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C72
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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

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; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
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; APPLICANT: Gerritsen, Mary E.
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; APPLICANT: Grimaldi, J. Christopher
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; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
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TITLE OF INVENTION: Acids Encoding the Same
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Query Match      100.0%; Score 2315; DB 3; Length 445;
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QY 121 LLFQPLWTFAILLFFVWLVAVLSLGTAGAAQVMGGQVEYKPLSGIRYMWSYHLIGLI 180
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QY 181 WTSEFILACQOMTITAGAVVTCYFNRSKNDDPPDHPILSSLSILFFYHQGTVVKGSFLISVV 240
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QY 241 RIPRIIVMYMGNALKEQOHCALSRFLFRCCYCCFWCLDKYLLHLNQNAVTTTAINGTDFC 300
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QY 421 NNARAOQDGHSLNEEGTELOAIVR 445
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RESULT 10

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US-09-997-653-177
; Sequence 177, Application US/09997653
; Patent No. 7034122
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.

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; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
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; APPLICANT: Gerber, Hanspeter
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; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC38
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; CURRENT FILING DATE: 2001-11-15
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 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/092182
 ; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 2315; DB 3; Length 445;
 Best Local Similarity 100.0%; Pred. No. 1.9e-241;
 Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Qy 121 LLFQPLWTFAILIFFFWVLVAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMWSYHLIGLI 180
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 Qy 181 WTSEFILACQOMTIAGAVTTCYFNRSKNDDPPDHPILSSLSILFFYHOGTVVKGSLISVV 240
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 Qy 241 RIPRIIWMYMONALKEQOHCALSRYLPRCCYCCFCWCLDKYLLHNONAYTTTAINGTDFC 300

Db 241 RIPRIIWMQNALKEQHGALSRYLPRCCVCCFWCLDKYLLHLNQNAVYTTAINGTDFC 300
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; Sequence 177, Application US/09989293A
; Patent No. 7034136
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
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; APPLICANT: Gurney, Austin L.
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; APPLICANT: Napier, Mary A.
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; APPLICANT: Paoni, Nicholas F.
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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C66
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 ; APPLICANT: Daniel E.H. Afar
 ; APPLICANT: Rene S. Hubert
 ; APPLICANT: Kahan Leong
 ; APPLICANT: Arthur B. Raitano
 ; APPLICANT: Douglas C. Safran
 ; TITLE OF INVENTION: NOVEL 13-TRANSMEMBRANE PROTEIN EXPRESSED
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 ; CURRENT FILING DATE: 2000-04-12
 ; EARLIER APPLICATION NUMBER: 60/128,858
 ; EARLIER FILING DATE: 1999-04-12
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 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 7
 ; LENGTH: 704
 ; TYPE: PRT
 ; ORGANISM: Human
 US-09-547-789-7

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 Qy 61 -----DLSIELDTE-----RNNMKCVLGFPAIVSTGITAVLLVILFVLKRRIKLTVE 106
 Db 287 EAGSDVSLVDLGFQTDPRVVLHLRQIW---LAFWILSILEVILLILFLRKRILTAIA 343

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		: : : : : : : : : : : : : : : : : :
Qy	154	-----VWEGQVQVEY-KPLSGIRYMWYSYHLGLIWTSSFIILA 188
		: : : : : : : : : : : : : : :
Db	404	KTCNPETFPSSHESQCPNARCQVYFGESGYTHRALGLQI---FNAAFWMFLANFVLA 460
		: : : : : : : : : : : : : : :
Qy	189	COQMTIAGAVVTCYFN-RSKNDPPDPHPILTSSLSILFFYHQGVTVVGSFLISVVVRIPIIV 247
		: : : : : : : : : : : : : : :
Db	461	LGQVTLAGAFASYWALRKPDPLPAFLPFSAGRALRYHTGSLAFGALILAIQVILIRVIL 520
		: : : : : : : : : : : : : : :
Qy	248	MYMNQALKSQOHALSRVLYFCRCYCCFWCLDKYLLHLNQNAYTTTAINGDTFCTSAKDAF 307
		: : : : : : : : : : : : : : :
Db	521	EYLDQRLKAAEN-KEAKCLMTCLKCCFWCLEKFIFLNRNAYIMAIYGTNFTCTSARNAF 579
		: : : : : : : : : : : : : : :
Qy	308	KILSKNSHFTSINCFGDPIFLGKVLVYCVTVGGLMAF-----NYN 350
		: : : : : : : : : : : : : : :
Db	580	FLLMRNIRIIRVAVLDKVTDFLLGLKLLIVGSV---GILAFFFTHRIIVQDTAPPLNY- 635
		: : : : : : : : : : : : : : :
Qy	351	RAFQWAVAPLLLVAFAYILVAHSFSLSVFETVLDALFLCFAVDLTNDGSSSEKPYFMDQEF 410
		: : : : : : : : : : : : : : :
Db	636	----YW-VPILVIVGSYLIHAHFFSVYGMCVDTILFLCFLEDLRNDGSAERYFYFMSSTL 690
		: : : : : : : : : : : : : : :
Qy	411	LSFVKRSNK 419
		: : : : : : : : : : : : : : :
Db	691	KKLLNKTNK 699
		: : : : : : : : : : : : : : :

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RESULT 13
US-10-104-047-3465
; Sequence 3465, Application US/10104047
; Patent No. 6943241
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. 6943241el full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3465
; LENGTH: 717
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-3465

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Query Match	24.3%	Score 563	DB 2	Length 717
Best Local Similarity	29.7%	Pred. No. 1.1e-51		
Matches 142	Conservative	87	Mismatches 171	Indels 78
Gaps				14

Qy	7	ILGLIALALSLAMMFTFRITTLVHIFISLVILGLFVCGV-LMWLYDYDTN-----	60
Db	246	LIGTLI-AMVLSWIFLLIRFLACLEWVF---MIGVIGIGYWHCYQYTNLQERP	300
Qy	61	-----DLSIELDTER--ENMKCVLGFALVSTGITAVLLVLIVLRKRKILTVELQIT	111
Db	301	SSVUTVYDIGIQTNISMYFELQQQTFMILCIIEVLIVLMILPLRNRIKVAILLKEG	360
Qy	112	NKAISSAPFLLFQPLWTFAILIFPFWLWVAVLLSLGTAGA-----	151
Db	361	SKAIGYVPSTLVYPALTFILLISICICYWVTVAVFLATSGVPVYKVIAPGGCHENQTC	420
Qy	152	-----AQVMSGGVVEKPLSG---IRYKMSYHLIG---IWTSEPTLACQMTIA	195
Db	421	PEIPNTTEIIAKACGFCALCNFAYCGKSLYHQIIFTFVYNLFPVLWLFNLVIALQCCAMA	480
Qy	196	GAUVTCYFNRSK-NDPDPHPILSSLSILFFYHQGTVVVKGSGFLISVRIPIRIVMYMQNAL	254
Db	481	GAFATYVWAMKKPPDIIRYPPTFAFGRAIRVHTGSLAFGSLLIIAIOFMKTVILEYDHLR	540

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255 KEQHQGALSRVLFRCCTCCFCLDKYLLHLNONTATTTAINGTDFCTCAKDAFKILSKNS 3114
541 KRTQN-TLSKFLQCLRCFCCWCLNKAIFLNRNAYIMIAIYGRNFCRSKDAFNLLMRNV 599
315 SHFTSINCFGDFIIFLGGKVLV-----VCFT-----VFGGLMAFNYNRAFOVWAVPL 360
600 LKVAVTDEVTVFVLFLGKLLVAGSIGVLAFUFFQRLPVIAQGASLNY-----YV-VPL 653
361 LLVAFFAYLVAHSFLSVFETVLDALFLCFAVDLETNDGSSSEKPYFMDQEFLSFVKRSN 418
654 LTVIFGSYLIANGFVSVMCVETIFCFLEDLERNDGSTARPYVVSQPLLKIFQEN 711

RESULT 14
US-09-547-789-2
; Sequence 2, Application US/095477789
; Patent No. 6943235
; GENERAL INFORMATION:
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Rene S. Hubert
; APPLICANT: Kahan Leong
; APPLICANT: Arthur B. Raitano
; APPLICANT: Douglas C. Safran
; TITLE OF INVENTION: NOVEL 13-TRANSMEMBRANE PROTEIN EXPRESSED
; TITLE OF INVENTION: IN PROSTATE CANCER
; FILE REFERENCE: 129.11USU1
; CURRENT APPLICATION NUMBER: US/09/547,789
; CURRENT FILING DATE: 2000-04-12
; EARLIER APPLICATION NUMBER: 60/128,858
; EARLIER FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 710
; TYPE: PRT
; ORGANISM: Human
US-09-547-789-2

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Query Match	23.3%;	Score 540;	DB 2;	Length 710;
Best Local Similarity	28.0%;	Pred. No. 3.2e-49;		
Matches	135;	Conservative	98;	Mismatches 160; Indels 90; Gaps 14
Qy	12	ILALALSIAWMFTFRFTITLLVHIFISIVILGGLFVCGVL--WMLYY-----	56	
Db	233	LVALGVALLSLLPILLRLVAGPLVLVILGVL--GVLAYGIYCWEEYRVLDRKGS	289	
Qy	57	----DYNDLSIELDTERENMKCVLGFAYVSTGTAVLLVLIFVLKRRIKUTVELFQITN	112	
Db	290	ISOLGFTNLISAYOSVQETWLAALIVLAV--LEAILLLMLIFLQRIARIAIALKES	345	
Qy	113	KAISSAPFLLPOPLWTFAILLIFFWLVAVLLSLGTAG-----AAOVMEGGQVEYKPL	165	
Db	346	KAVQOMSTWFYPLVTFVLLILICITAYWMTALYILATSGOPYVLWASNISSPG-CEKVP	404	
Qy	166	S-----GIRYMS-----YHLGLIWTSEFILAQQMT	193	
Db	405	NTSCNPHTALVNSSCPGLMCFQGYSGKGLTQRSVFNLIQIYGVGLFTLWNLVAGQCV	464	
Qy	194	IAGAVTCYENRSK-NPPDPHPILSSLSILFFYHOGTVVKVSGSFLISVVRIPIIWMON	252	
Db	465	LAFAPSYWAFHKPDIPFPPLISAFIRTLRYHTGSLAFQALILTLVQIARVILEYIDH	524	
Qy	253	ALKEBQHGALSRYLFRCCYCCFWCLDKYLLHLNQAYTTTITAINGDPDCTSAKDAPKILSK	312	
Db	525	KLRGVQN-PPVARCIIMCCFKCMLWCLEKFIKPLBNNAVITMIAIYGNKFCVSAKNAPMLLMR	583	
Qy	313	NSSHFTSINCFGDFIILFGKVLVV-----CFTVFGGLMA-----FYNRAFOVM	356	
Db	584	NIVRVVLDDKTDULLFLGKLLVGGVGVLSPFFPSGRIPGLGDKDFKSPHLY-----YW	638	
Qy	357	AVPILLVAFFAYLVHAHSFLSVFETVLDAFLFCFADVLDETNDGSSSEKPYEMDOEFLSFVKR	416	
Db	639	-LPMTSILGAYVTIASGFFSVFGMCDVTLFLCFLEDLERNNGSLDRPYNGSKLLKIILGK	697	

Job time : 53 secs

Qy 417 SNK 419
|:
Db 698 KNE 700

RESULT 15

US-09-547-789-5
; Sequence 5, Application US/09547789
; Patent No. 6943235
; GENERAL INFORMATION:
; APPLICANT: Daniel E. H. Afar
; APPLICANT: Rene S. Hubert
; APPLICANT: Kahan Leong
; APPLICANT: Arthur B. Raitano
; APPLICANT: Douglas C. Saffran
; TITLE OF INVENTION: NOVEL 13-TRANSMEMBRANE PROTEIN EXPRESSED
; FILE REFERENCE: 129.11USUI
; CURRENT APPLICATION NUMBER: US/09/547,789
; EARLIER FILING DATE: 2000-04-12
; EARLIER APPLICATION NUMBER: 60/128,858
; EARLIER FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 705
; TYPE: PRT
; ORGANISM: Mouse
US-09-547-789-5

Query Match 23.3%; Score 538.5; DB 2; Length 705;
Best Local Similarity 27.7%; Pred. No. 4.6e-49;
Matches 133; Conservative 87; Mismatches 174; Indels 87; Gaps 9;
Qy 12 ILALALSMMFTRFITLLVHIFISLVILGLLFVC--GVL-WLLYYDYTNDSIELDT 68
Db 229 LVALGVALSLFLFILLRLVAAPLVLLLVGLVAVLAYGIYHCWQQYQVFRDKGASITQ 288
Qy 69 ERENMKCVLGFA-----IVSTGITAVLLVLPVLRKRIKLTVELFQIT 111
Db 289 -----LGFTNFSAYQSVKETWLAALIVLAVLEGILLMLLIFLQRIAIALLKEA 340
Qy 112 NKAISSAPFLLOPLWTFAILIFFWVLWVAVLLSLGTAGAAQ----- 153
Db 341 SRAVGQMMSTMFPLVTFVLLVICIGYVAVTALYATSGQPQIYMASNTSTPCENVPV 400
Qy 154 -----VMEGQVEYKPLSGIRYMWVSYHLGLIWTSEFILACQMTI 194
Db 401 NMTCDPMAPLNSCPNLKCVFKGYSTTGLAQRSLFNLQIYGVGLFWTVNVLALGQCVL 460
Qy 195 AGAVVTCYFNRSK-NDPPDHPILSSLSILFFYHOGTVVKGSEFLISVVRIPIIIVMYMNA 253
Db 461 AGAFASYWAFHKPRDPTTFLSSAPRTLYRTGSLAFGALILSLVQIARVILEYIDHK 520
Qy 254 LKEQQHGALSKYLFRCYCCFWCLDKYLLHLNQNAVTTTAINGTDFCTSAKDAFKILSKN 313
Db 521 LRGSQN-PVARIICCFKCLWCLEKFIKFLNRNAVIMAIYGNKFCVSAKNAFMLLMRN 579
Qy 314 SSHFTSINCFGDFIIFLGKVLVVCFTVFGGLMAPNY-----NRAFQWAV 358
Db 580 VLRVVLVDKVTDLVLLFFGKLLV-----GGVGVLSFFFSGRIKGLGKDFENPNLYYL 634
Qy 359 PLLLVAFAYLVAFSLVSVFETVLDALFLCFVADLETNDGSEKPYEMDOEFLSFVKRSN 418
Db 635 PIMTSIMGAIVIASGFFSVFGMCVDTLFLCFLEDLERNDGSEKPYPMKALLKILGKN 694
Qy 419 K 419
Db 695 E 695

Search completed: June 6, 2006, 22:06:39

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